



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁵ : C12N 15/62, 1/19, 1/20, 11/16 // 1:19, C12R 1:465</p>	<p>A1</p>	<p>(11) International Publication Number: WO 94/18330 (43) International Publication Date: 18 August 1994 (18.08.94)</p>
<p>(21) International Application Number: PCT/EP94/00427 (22) International Filing Date: 10 February 1994 (10.02.94) (30) Priority Data: 93200350.2 10 February 1993 (10.02.93) NL (71) Applicant (for AU BB CA GB IE LK MN MW NZ SD only): UNILEVER PLC [GB/GB]; Unilever House, Blackfriars, London EC4 4BQ (GB). (71) Applicant (for all designated States except AU BB CA GB IE LK MN MW NZ SD US): UNILEVER N.V. [NL/NL]; Veena 455, NL-3013 AL Rotterdam (NL). (72) Inventors; and (75) Inventors/Applicants (for US only): FRENKEN, Leon, Gerardus, J. [NL/NL]; Geldersestraat 90, NL-3011 MP Rotterdam (NL). DE GEUS, Pieter [NL/NL]; Boeier 24, NL-2991 KB Barendrecht (NL). KLIS, Franciscus, Maria [NL/NL]; Benedenlang 102, NL-1025 KL Amsterdam (NL). TOSCHKA, Holger, York [DE/DE]; Langueso-Iglo, BR3, Aeckern 1, D-48734 Reken (DE). VERRIPS, Cornelis, Theodorus [NL/NL]; Hagedoorn 18, NL-3142 KB Maassluis (NL).</p>		<p>(81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</p>
<p>(54) Title: IMMOBILIZED PROTEINS WITH SPECIFIC BINDING CAPACITIES AND THEIR USE IN PROCESSES AND PRODUCTS (57) Abstract A method is provided for immobilizing a binding protein capable of binding to a specific compound, using recombinant DNA techniques for producing said binding protein or a functional part thereof. The binding protein is immobilized by producing it as part of a chimeric protein also comprising an anchoring part derivable from the C-terminal part of an anchoring protein, thereby ensuring that the binding protein is localized in or at the exterior of the cell wall of the host cell. Suitable anchoring proteins are yeast α-agglutinin, FLO1 (a protein associated with the flocculation phenotype in <i>S. cerevisiae</i>), the Major Cell Wall Protein of lower eukaryotes, and a proteinase of lactic acid bacteria. For secretion the chimeric protein can comprise a signal peptide including those of α-mating factor of yeast, α-agglutinin of yeast, invertase of <i>Saccharomyces</i>, inulinase of <i>Kluyveromyces</i>, α-amylase of <i>Bacillus</i>, and proteinase of lactic acid bacteria. Also provided are recombinant polynucleotides encoding such chimeric protein, vectors comprising such polynucleotide, transformed microorganisms having such chimeric protein immobilized on their cell wall, and a process for carrying out an isolation process by using such transformed host, wherein a medium containing said specific compound is contacted with such host cell to form a complex, separating said complex from the medium and, optionally, releasing said specific compound from said binding protein.</p>		

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Title: Immobilized proteins with specific binding capacities and their use in
 processes and products

Background of the invention

5 The pharmaceutical, the fine chemicals and the food industry need a number of
compounds that have to be isolated from complex mixtures such as extracts of
animal or plant tissue, or fermentation broth. Often these isolation processes
determine the price of the product.

Conventional isolation processes are not very specific and during the isolation
10 processes the compound to be isolated is diluted considerably with the consequence
that expensive steps for removing water or other solvents have to be applied.

For the isolation of some specific compounds affinity techniques are used. The
advantage of these techniques is that the compounds bind very specifically to a
15 certain ligand. However these ligands are quite often very expensive.

To avoid spillage of these expensive ligands they can be linked to an insoluble
support. However, often linking the ligand is also expensive and, moreover, the
functionality of the ligand is often affected negatively by such procedure.

So a need exists for developing cheap processes for preparing highly effective
20 immobilized ligands.

Summary of the invention

The invention provides a method for immobilizing a binding protein capable of
binding to a specific compound, comprising the use of recombinant DNA techniques
25 for producing said binding protein or a functional part thereof still having said
specific binding capability, said protein or said part thereof being linked to the
outside of a host cell, whereby said binding protein or said part thereof is localized
in the cell wall or at the exterior of the cell wall by allowing the host cell to produce
and secrete a chimeric protein in which said binding protein or said functional part
30 thereof is bound with its C-terminus to the N-terminus of an anchoring part of an
anchoring protein capable of anchoring in the cell wall of the host cell, which
anchoring part is derivable from the C-terminal part of said anchoring protein.

Preferably, the host is selected from Gram-positive bacteria and fungi, which have a cell wall at the outside of the host cell, in contrast to Gram-negative bacteria and cells of higher eukaryotes such as animal cells and plant cells, which have a membrane at the outside of their cells. Suitable Gram-positive bacteria comprise lactic acid bacteria and bacteria belonging to the genera *Bacillus* and *Streptomyces*. Suitable fungi comprise yeasts belonging to the genera *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* and *Saccharomyces*, and moulds belonging to the genera *Aspergillus*, *Penicillium* and *Rhizopus*. In this specification the group of fungi comprises the group of yeasts and the group of moulds, which are also known as lower eukaryotes. In contrast to the cells in plants and animals, the group of bacteria and lower eukaryotes are also indicated in this specification as microorganisms.

The invention also provides a recombinant polynucleotide capable of being used in a method as described above, such polynucleotide comprising (i) a structural gene encoding a binding protein or a functional part thereof still having the specific binding capability, and (ii) at least part of a gene encoding an anchoring protein capable of anchoring in the cell wall of a Gram-positive bacterium or a fungus, said part of a gene encoding at least the anchoring part of said anchoring protein, which anchoring part is derivable from the C-terminal part of said anchoring protein.

The anchoring protein can be selected from α -agglutinin, a-agglutinin, FLO1, the Major Cell Wall Protein of a lower eukaryote, and proteinase of lactic acid bacteria.

Preferably, such polynucleotide further comprises a nucleotide sequence encoding a signal peptide ensuring secretion of the expression product of the polynucleotide, which signal peptide can be derived from a protein selected from the α -mating factor of yeast, α -agglutinin of yeast, invertase of *Saccharomyces*, inulinase of *Kluyveromyces*, α -amylase of *Bacillus*, and proteinase of lactic acid bacteria. The polynucleotide can be operably linked to a promoter, which is preferably an inducible promoter.

The invention further provides a recombinant vector comprising a polynucleotide according to the invention, a chimeric protein encoded by a polynucleotide according to the invention, and a host cell having a cell wall at the outside of its cell and containing at least one polynucleotide according to the invention. Preferably at least one polynucleotide is integrated in the chromosome of the host cell. Another

embodiment of this part of the invention is a host cell having a chimeric protein according to the invention immobilized in its cell wall and having the binding protein part of the chimeric protein localized in the cell wall or at the exterior of the cell wall.

- 5 Another embodiment of the invention is a process for carrying out an isolation process by using an immobilized binding protein or functional part thereof still capable of binding to a specific compound, wherein a medium containing said specific compound is contacted with a host cell according to the invention under conditions whereby a complex between said specific compound and said immobilized
10 binding protein is formed, separating said complex from the medium originally containing said specific compound and, optionally, releasing said specific compound from said binding protein or functional part thereof.

Brief description of the figures

- 15 In Figure 1 the composition of pEMBL9-derived plasmid pUR4122 is indicated, the preparation of which is described in Example 1.
- In Figure 2 the composition of plasmid pUR2741 is indicated, which is a derivative of published plasmid pUR2740, see Example 1.
- In Figure 3 the composition of pEMBL9-derived plasmid pUR2968 is indicated. Its
20 preparation is described in Example 1.
- In Figure 4 the preparation of plasmid pUR4174 starting from plasmids pUR2741, pUR2968 and pUR4122 is indicated, as well as the preparation of plasmid pUR4175 starting from plasmids pSY16, pUR2968 and pUR4122. These preparations are described in Example 1.
- 25 In Figure 5 the composition of plasmid pUR2743.4 is indicated. Its preparation is described in Example 2. It contains the 714 bp *Pst*I-*Xho*I fragment given in SEQ ID NO: 12, which fragment encodes an scFv-TRAS fragment of anti-traseolide® antibody 02/01/01.
- In Figure 6 the composition of plasmid pUR4178 is indicated. Its preparation is
30 indicated in Example 2. It contains the above mentioned 714 bp *Pst*I-*Xho*I fragment given in SEQ ID NO: 12. This plasmid is suitable for the expression of a fusion

protein between scFv-TRAS and α AGG preceded by the invertase signal sequence (SUC2).

In Figure 7 the composition of plasmid pUR4179 is indicated. Its preparation is indicated in Example 2. It contains the above mentioned 714 bp *PstI-XhoI* fragment
5 given in SEQ ID NO: 12. This plasmid is suitable for the expression of a fusion protein between scFv-TRAS and α AGG preceded by the prepro- α -mating factor signal signal sequence.

In Figure 8 a molecular design picture is given, showing the musk odour molecule traseolide® and a modified musk antigen, described in Example 3.

10 In Figure 9 the composition of plasmid pUR4177 is indicated. Its construction is described in Example 4. Plasmid pUR4177 contains the 734 bp *EagI-XhoI* DNA fragment given in SEQ ID NO: 13 encoding the variable regions of the heavy and light chain fragments from the monoclonal antibody directed against the human chorionic gonadotropin (an scFv-HCG fragment) and is a 2 μ m-based vector
15 suitable for production of the chimeric scFv HCG- α AGG fusion protein preceded by the invertase signal sequence and under the control of the GAL7 promoter.

In Figure 10 the composition of plasmid pUR4180 is indicated. Its preparation is indicated in Example 4. It contains the above mentioned 734 bp *EagI-XhoI* DNA fragment given in SEQ ID NO: 13 and is a 2 μ m-based vector suitable for
20 production of the chimeric scFv-HCG- α AGG fusion protein preceded by the prepro- α -mating factor signal sequence and under the control of the GAL7 promoter.

In Figure 11 the composition of plasmid pUR2990, a 2 μ m-based vector, is indicated, which is suggested in Example 5 as a starting vector for the preparation of plasmid pUR4196 (see Figure 12). Plasmid pUR2990 contains a DNA fragment
25 encoding a chimeric lipase-FLO1 protein that will be anchored in the cell wall of a lower eukaryote and can catalyze lipid hydrolysis.

In Figure 12 the composition of plasmid pUR4196 is indicated. Its preparation is explained in Example 5. It contains a DNA fragment encoding a chimeric protein comprising the scFv-HCG followed by the C-terminal part of the FLO1-protein, and
30 is a vector suitable for the production of a chimeric protein anchored in the cell wall of the host organism and can bind HCG.

In Figure 13 the composition of plasmid pUR2985 is indicated. Its preparation is described in Example 6. It contains a *choB* gene coding for the mature part of the cholesterol oxidase (EC 1.1.3.6) obtained via PCR techniques from the chromosome of *Brevibacterium sterolicum*.

- 5 In Figure 14 the composition of plasmid pUR2987 is indicated. Its preparation from plasmid pUR2985 is described in Example 6. It contains a DNA sequence comprising the *choB* gene coding for the mature part of the cholesterol oxidase preceded by DNA encoding the prepro- α -mating factor signal sequence and followed by DNA encoding the C-terminal part of α -agglutinin.
- 10 In Figure 15 the composition of the published plasmid pGKV550 is indicated. It is described in Example 7 and contains the complete cell wall proteinase operon of *Lactococcus lactis* subsp. *cremoris* Wg2, including the promoter, the ribosome binding site and the *prtP* gene.

In Figure 16 the composition of plasmid pUR2988 is indicated. Its preparation is
15 described in Example 7. It is anticipated that this plasmid can be used for preparing a further plasmid pUR2989, which after introduction in a lactic acid bacterium will be responsible for producing a chimeric protein that will be anchored at the outer surface of the lactic acid bacterium and is capable of binding cholesterol.

In Figure 17 the composition of plasmid pUR2993 is indicated. Its preparation is
20 described in Example 8. It is anticipated that this plasmid can be used for transforming yeast cells that can bind a human epidermal growth factor (EGF) through an anchored chimeric protein containing an EGF receptor.

In Figure 18 the composition of plasmids pUR4482 and 4483 is indicated. Their preparation is described in Example 9. Plasmid pUR4482 is a yeast episomal
25 expression plasmid for expression of a fusion protein with the invertase signal sequence, the CH_v09 variable region, the Myc-tail, and the "X-P-X-P" Hinge region of a camel antibody, and the α -agglutinin cell wall anchor region. Plasmid pUR4483 differs from pUR4482 in that it does not contain the "X-P-X-P" Hinge region.

In Figure 19 immunofluorescent labelling (anti-Myc antibody) of SU10 cells in the
30 exponential phase ($OD_{530}=0.5$) expressing the genes of camel antibodies present on plasmids pUR4424, pUR4482 and pUR4483 is shown.

Ph = phase contrast, Fl = fluorescence.

In Figure 20 immunofluorescent labelling (anti-human IgG antibody) of SU10 cells in the exponential phase ($OD_{530}=0.5$) expressing the genes of camel antibodies present on plasmids pUR4424, pUR4482 and pUR4483 is shown.

Ph = phase contrast, Fl = fluorescence.

5

Abbreviations used in the Figures:

	α -gal:	gene encoding guar α -galactosidase
	AG-alpha-1/AG α 1:	gene expressing α -agglutinin from <i>S. cerevisiae</i>
	AG α 1 cds/ α -AGG:	coding sequence of α -agglutinin
10	Amp/amp r:	β -lactamase resistance gene
	CHv09:	camel heavy chain variable 09 fragment
	EmR:	erythromycin resistance gene
	fl:	phage fl replication sequence
	FLO1/FLO (C-part):	C-terminal part of FLO1 coding sequence of flocculation
15		protein
	Hinge:	Camel "X-P-X-P" Hinge region, see Example 9
	LEU2:	<i>LEU2</i> gene
	LEU2d/Leu2d:	truncated <i>LEU2</i> gene
	Leu 2d cs:	coding sequence <i>LEU2d</i> gene
20	MycT:	camel Myc-tail
	Ori MB1:	origin of replication MB1 derived from <i>E. coli</i> plasmid
	Pgal7/pGAL7:	<i>GAL7</i> promoter
	Tpgk:	terminator of the phosphoglyceratekinase gene
	pp α -MF/MF α 1ss:	prepro-part of α -mating factor (= signal sequence)
25	repA:	gene encoding the repA protein required for replication (Fig. 15/16).
	ScFv (Vh-Vl):	single chain antibody fragment containing V _H and V _L chains
	ss:	signal sequence
	SUC2:	invertase signal sequence
30	2u/2 micron:	2 μ m sequence

Detailed description of the invention

The present invention relates to the isolation of valuable compounds from complex mixtures by making use of immobilized ligands. The immobilized ligands can be proteins obtainable via genetic engineering and can consist of two parts, namely
5 both an anchoring protein or functional part thereof and a binding protein or functional part thereof.

The anchoring protein sticks into cell walls of microorganisms, preferably lower eukaryotes, e.g. yeasts and moulds. Often this type of proteins has a long C-terminal
10 part that anchors it in the cell wall. These C-terminal parts have very special amino acid sequences. A typical example is anchoring via C-terminal sequences of proteins enriched in proline, see Kok (1990).

The C-terminal part of these anchoring proteins can contain a substantial number of potential serine and threonine glycosylation sites. O-glycosylation of these sites gives
15 a rod-like conformation to the C-terminal part of these proteins.

In the case of anchored manno-proteins they seem to be linked to the glucan in the cell wall of lower eukaryotes, as they cannot be extracted from the cell wall with sodium dodecyl sulphate (SDS), but can be liberated by glucanase treatment, see
our co-pending patent application WO-94/01567 (UNILEVER) published 20 January
20 1994 and Schreuder c.s. (1993), both being published after the claimed priority date. Another mechanism to anchor proteins at the outer side of a cell is to make use of the property that a protein containing a glycosyl-phosphatidyl-inositol (GPI) group anchors via this GPI group to the cell surface, see Conzelmann c.s. (1990).

25 The binding protein is so called, because it ligates or binds to the specific compound to be isolated. If the N-terminal part of the anchoring protein is sufficiently capable of binding to a specific compound, the anchoring protein itself can be used in a process for isolating that specific compound. Suitable examples of a binding protein comprise an antibody, an antibody fragment, a combination of antibody fragments, a
30 receptor protein, an inactivated enzyme still capable of binding the corresponding substrate, and a peptide obtained via Applied Molecular Evolution, see Lewin (1990), as well as a part of any of these proteinaceous substances still capable of

binding to the specific compound to be isolated. All these binding proteins are characterized by specific recognition of the compounds or group of related compounds to be isolated. The binding rate and release rate, and therefore the binding constant between the specific compound to be isolated and the binding protein, can be regulated either by changing the composition of the liquid extract in which the compound is present or, preferably, by changing the binding protein by protein engineering.

The gene coding for the chimeric protein comprising both the binding protein and the anchoring protein (or functional parts thereof) can be placed under control of a constitutive, inducible or derepressible promoter and will generally be preceded by a DNA fragment encoding a signal sequence ensuring efficient secretion of the chimeric protein. Upon secretion the chimeric protein will be anchored in the cell wall of the microorganisms, thereby covering the surface of the microorganisms with the chimeric protein. These microorganisms can be obtained in normal fermentation processes and their isolation is a cheap process, when physical separation processes are used, e.g. centrifugation or membrane filtration.

After washing, the isolated microorganisms can be added to liquid extracts containing the valuable specific compound or compounds. After some time the equilibrium between the bound and free specific compound(s) will be reached and the microorganisms to which the specific compound or group of related compounds is bound can be separated from the extract by simple physical techniques.

Alternatively, the microorganisms covered with ligands can be brought on a support material and subsequently this coated support material can be used in a column. The liquid extract containing the specific compound or compounds of interest can be added to the column and afterwards the compound(s) can be released from the ligand by changing the composition of the eluting liquid or the temperature or both. A skilled person will recognize that in addition to these two possibilities other modifications can be used for effecting the binding of the specific compound and the ligand, their subsequent isolation and/or the release of the specific compound(s). In particular the invention relates to chimeric proteins that are bound to the cell wall of lower eukaryotes. Suitable lower eukaryotes comprise yeasts, e.g. *Candida*,

Debaryomyces, *Hansenula*, *Kluyveromyces*, *Pichia* and *Saccharomyces*, and moulds e.g. *Aspergillus*, *Penicillium* and *Rhizopus*. For some applications prokaryotes are also applicable, especially Gram-positive bacteria, examples of which include lactic acid bacteria, and bacteria belonging to the genera *Bacillus* and *Streptomyces*.

5

For lower eukaryotes the present invention provides genes encoding chimeric proteins consisting of:

- a. a DNA sequence encoding a signal sequence functional in a lower eukaryotic host, e.g. derived from a yeast protein including the α -mating factor, invertase,
10 α -agglutinin, inulinase or derived from a mould protein e.g. xylanase;
- b. a structural gene encoding a C-terminal part of a cell wall protein preceded by a structural gene encoding a protein, that is capable of binding to the specific compound or group of compounds of interest, examples of which include
 - an antibody,
 - 15 - a single chain antibody fragment (scFv; see Bird and Webb Walker (1991),
 - a variable region of the heavy chain (V_H) or a variable region of the light chain (V_L) of an antibody or that part of such variable region still containing one to three of the complementarity determining regions (CDRs),
 - an agonist-recognizing part of a receptor protein or a part thereof still capable
20 of binding the agonist,
 - a catalytically inactivated enzyme, or a fragment of such enzyme still containing a substrate binding site of the enzyme,
 - specific lipid binding proteins or parts of these proteins still containing the lipid binding site(s), see Ossendorp (1992), and
 - 25 - a peptide that has been obtained via Applied Molecular Evolution, see Lewin (1990).

All expression products of these genes are characterized in that they consists of a signal sequence and both a protein part, that is capable of binding to the compound(s) to be isolated, and a C-terminus of a typically cell wall bound protein,
30 examples of the latter including α -agglutinin, see Lipke c.s. (1989), α -agglutinin, see Roy c.s. (1991), FLO1 (see Example 5 and SEQ ID NO: 14) and the Major Cell

Wall Protein of lower eukaryotes, which C-terminus is capable of anchoring the expression product in the cell wall of the lower eukaryote host organism.

The expression of these genes encoding chimeric proteins can be under control of a constitutive promoter, but an inducible promoter is preferred, suitable examples of which include the GAL7 promoter from *Saccharomyces*, the inulinase promoter from *Kluyveromyces*, the methanol-oxidase promoter from *Hansenula*, and the xylanase promoter of *Aspergillus*. Preferably the constructs are made in such a way that the new genetic information is integrated in a stable way in the chromosome of the host cell, see e.g. WO-91/00920 (UNILEVER).

10 The lower eukaryotes transformed with the above mentioned genes can be grown in normal fermentation, continuous fermentation, or fed batch fermentation processes.

The selection of a suitable process for growing the microorganism will depend on the construction of the gene and the promoter used, and on the desired purity of the cells after the physical separation procedure(s).

15

For bacteria the present invention deals with genes encoding chimeric proteins consisting of:

- a. a DNA sequence encoding a signal sequence functional in the specific bacterium, e.g. derived from a *Bacillus* α -amylase, a *Bacillus subtilis* subtilisin, or a *Lactococcus lactis* subsp. *cremoris* proteinase;
 - 20 b. a structural gene encoding a C-terminal part of a cell wall protein preceded by a structural gene encoding a protein capable of binding to the specific compound or group of compounds of interest, examples of which are given above for a lower eukaryote.
- 25 All expression products of these genes are characterized in that they consist of a signal sequence and both a protein part, that is capable of binding to the specific compound or specific group of compounds to be isolated, and a C-terminus of a typically cell wall-bound protein such as the proteinase of *Lactococcus lactis* subsp. *cremoris* strain Wg2, see Kok c.s. (1988) and Kok (1990), the C-terminus of which is
- 30 capable of anchoring the expression product in the cell wall of the host bacterium.

The invention is illustrated with the following Examples without being limited thereto. First the endonuclease restriction sites mentioned in the Examples are given.

5	<i>BstEII</i>	G GTNACC CCANTG G	<i>ClaI</i>	AT CGAT TAGC TA	<i>EagI</i>	C GGCCG GCCGG C
10	<i>EcoRI</i>	G AATTC CTTAA G	<i>HindIII</i>	A AGCTT TTCGA A	<i>NheI</i>	G CTAGC CGATC G
	<i>NotI</i>	GC GGCCGC CGCCGG CG	<i>NruI</i>	TCG CGA AGC GCT	<i>PstI</i>	CTGCA G G ACGTC
15	<i>SacI</i>	GAGCT C C TCGAG	<i>SalI</i>	G TCGAC CAGCT G	<i>XhoI</i>	C TCGAG GAGCT C

Example 1. Construction of a gene encoding a chimeric protein that will be anchored in the cell wall of a lower eukaryote and is able to bind with high specificity lysozyme from a complex mixture.

Lysozyme is an anti-microbial enzyme with a number of applications in the pharmaceutical and food industries. Several sources of lysozyme are known, e.g. egg yolk or a fermentation broth containing a microorganism producing lysozyme.

Monoclonal antibodies have been raised against lysozyme, see Ward c.s. (1989), and the mRNA's encoding the light and heavy chains of such antibodies have been isolated from the hybridoma cells and used as template for the synthesis of cDNA using reverse transcriptase. Starting from the plasmids as described by Ward c.s. (1989), we constructed a pEMBL-derived plasmid, designated pUR4122, in which the multiple cloning site of the pEMBL-vector, ranging from the *EcoRI* to the *HindIII* site, was replaced by a 231 bp DNA fragment, whose nucleotide sequence is given in SEQ ID NO: 1 and has an *EcoRI* site (GAATTC) at nucleotides 1-6, a *PstI* site (CTGCAG) at nucleotides 105-110, a *BstEII* site (GGTCACC) at nucleotides 122-128, a *XhoI* site (CTCGAG) at nucleotides 207-212, and a *HindIII* site (AAGCTT) at nucleotides 226-231.

Construction of pUR4122

Plasmid pEMBL9, see Dente c.s. (1983), was digested with *EcoRI* and *HindIII* and the resulting large fragment was ligated with the double stranded synthetic DNA fragment given in SEQ ID NO: 1. For the successive ligation of DNA fragments, which finally form the coding sequence of a single chain antibody fragment for lysozyme, the following elements were combined in the 231 bp DNA fragment (SEQ ID NO: 1) inserted into the pEMBL-9 vector: the 3' part of the GAL7 promoter, the invertase signal sequence (SUC2), a *PstI* restriction site, a *BstEII* restriction site, a sequence encoding the (GGGGS)₃ peptide linker connecting the V_H and V_L fragments, a *SacI* restriction site, a *XhoI* restriction site and a *HindIII* restriction site, resulting in plasmid pUR4119. To obtain the in frame fusion between V_H and the GGGGS-linker plasmid pSW1-VHD1.3-VKD1.3-TAG1, see Ward c.s. (1989), was digested with *PstI* and *BstEII* and a DNA fragment of 0.35 kbp was ligated in the correspondingly digested pUR4119 resulting in plasmid pUR4119A. Subsequently the plasmid pSW1-VHD1.3-VKD1.3-TAG1 was digested with *SacI* and *XhoI* and this fragment containing the coding part of V_L was finally ligated into the *SacI/XhoI* sites of pUR4119A, resulting in plasmid pUR4122 (see Figure 1).

Construction of pUR4174, see Figure 4

To obtain *S. cerevisiae* episomal expression plasmids containing DNA encoding a cell wall anchor derived from the C-terminal part of α -agglutinin, plasmid pUR2741 (see Figure 2) was selected as starting vector. Basically, this plasmid is a derivative of pUR2740, which is a derivative of plasmid pUR2730 as described in WO-91/19782 (UNILEVER) and by Verbakel (1991). The preparation of pUR2730 is clearly described in Example 9 of EP-A1-0255153 (UNILEVER). Plasmid pUR2741 differs from plasmid pUR2740 in that the *EagI* restriction site within the remaining part of the already inactive *tet* resistance gene was deleted through *NruI/SalI* digestion. The *SalI* site was filled in prior to religation.

After digesting pUR4122 with *SacI* (partially) and *HindIII*, the approximately 800 bp fragment was isolated and cloned into the pUR2741 vector fragment, which was

obtained after digestion of pUR2741 with the same enzymes. The resulting plasmid was named pUR4125.

A plasmid named pUR2968 (see Figure 3) was made by (1) digesting with *Hind*III the *Agα1*-containing plasmid pLα21 published by Lipke c.s. (1989), (2) isolating an
5 about 6.1 kbp fragment and (3) ligating that fragment with *Hind*III-treated pEMBL9, so that the 6.1 kbp fragment was introduced into the *Hind*III site present in the multiple cloning site of the pEMBL9 vector.

Plasmid pUR4125 was digested with *Xho*I and *Hind*III and the about 8 kbp fragment was ligated with the approximately 1.4 kbp *Nhe*I-*Hind*III fragment of
10 pUR2968, using *Xho*I/*Nhe*I adapters having the following sequence:

<i>Xho</i> I	<i>Nhe</i> I	
5' - <u>TC GAG</u> ATC AAA GGC GGA TCT <u>G</u> - 3'		= SEQ ID NO: 2
3' - <u>C</u> TAG TTT CCG CCT AGA <u>CGATC</u> - 5'		= SEQ ID NO: 3.

The plasmid resulting from the ligation of the appropriate parts of plasmids
15 pUR2968, pUR4125 and *Xho*I/*Nhe*I adapters, was designated pUR4174 and encodes a chimeric fusion protein at the amino terminus consisting of the invertase signal (pre) peptide, followed by the scFv-LYS polypeptide and, finally, the C-terminal part of α-agglutinin (see Figure 4).

20 Construction of pUR4175, see Figure 4

Upon digesting pUR4122 (see above) with *Pst*I and *Hind*III, the approximately 700 bp fragment was isolated and ligated into a vector fragment of plasmid pSY16, see Harmsen c.s. (1993), which was digested with *Eag*I and *Hind*III and using
*Eag*I-*Pst*I adapters, having the following sequence:

<i>Eag</i> I	<i>Pst</i> I	
5' - <u>G GCC GCC</u> CAG GTG CAG <u>CTG CA</u> - 3'		= SEQ ID NO: 4
3' - <u>CGG GTC CAC GTC</u> <u>G</u> - 5'		= SEQ ID NO: 5

The resulting plasmid, named pUR4132, was digested with *Xho*I and *Hind*III and ligated with the approximately 1.4 kbp *Nhe*I-*Hind*III fragment of pUR2968 (see
30 above), using *Xho*I/*Nhe*I adapters as described above, resulting in pUR4175 (see Figure 4). This plasmid contains a gene encoding a chimeric protein consisting of the α-mating factor prepro-peptide, followed by the scFv-LYS polypeptide and, finally, the C-terminal part of α-agglutinin.

Example 2. Construction of genes encoding a series of homologous chimeric proteins that will be anchored in the cell wall of a lower eukaryote and are able to bind with high specificities the musk fragrance trascolide® from a complex mixture.

5 The isolation of RNA from the hybridoma cell lines, the preparation of cDNA and amplification of gene fragments encoding the variable regions of antibodies by PCR was performed according to standard procedures known from the literature, see e.g. Orlandi c.s. (1989). For the PCR amplification different oligonucleotide primers have been used.

10 For the heavy chain fragment:

A: AGG TSM ARC TGC AGS AGT CWG G = SEQ ID NO: 6
PstI

in which S is C or G, M is A or C, R is A or G, and W is A or T,
and

15 B: TGA GGA GAC GGT GAC CGT GGT CCC TTG GCC CC = SEQ ID NO: 7.
BstEII

For the light chain fragment (Kappa):

C: GAC ATT GAG CTC ACC CAG TCT CCA = SEQ ID NO: 8,
SacI

20 and

D: GTT TGA TCT CGA GCT TGG TCC C = SEQ ID NO: 9.
XhoI

Construction of pUR4143

25 To simplify future construction work an *EagI* restriction site was introduced in pUR4122 (see above), at the junction between the invertase signal sequence and the scFv-LYS. This was achieved by replacing the about 110 bp *EcoRI*-*PstI* fragment within the synthetic fragment given in SEQ ID NO: 1 by synthetic adapters with the following sequence:

30 *EcoRI* *PstI*
AATTCGGCCGTTCAAGTGCAGCTGCA = SEQ ID NO: 10
GCCGGCAAGTCCACGTCG = SEQ ID NO: 11.

The resulting plasmid was designated pUR4122.1: a construction vector for single chain Fv assembly in frame behind an *EagI* site for expression behind either the prepro- α -mating factor sequence or the SUC2 invertase signal sequence.

After digesting the heavy chain PCR fragment with *PstI* and *BstEII*, two fragments
5 were obtained: a *PstI* fragment of about 230 bp and a *PstI/BstEII* fragment of about 110 bp. The latter fragment was cloned into vector pUR4122.1, which was digested with *PstI* and *BstEII*. The newly obtained plasmid (pUR4122.2) was digested with *SacI* and *XhoI*, after which the light chain PCR fragment (digested with the same restriction enzymes) was cloned into the vector, resulting in pUR4122.3. This
10 plasmid was digested with *PstI*, after which the above described about 230 bp *PstI* fragment was cloned into the plasmid vector, resulting in a plasmid called pUR4143. Two orientations are possible, but selection can be made by restriction analysis, as usual. Instead of the scFv-LYS gene originally present in pUR4122, this new plasmid pUR4143 contains a gene encoding an scFv-TRAS fragment of anti-traseolide
15 antibody 02/01/01 (for the nucleotide sequence of the 714 bp *PstI-XhoI* fragment see SEQ ID NO: 12).

Construction of pUR4178 and pUR4179.

After digesting pUR4143 with *EagI* and with *HindIII*, an about 715 bp fragment can
20 be isolated. Subsequently, this fragment can be cloned into the vector backbone fragments of pUR2741 and pUR4175, that were digested with the same restriction enzymes. In the case of pUR2741, this resulted in plasmid pUR2743.4 (see Figure 5). This plasmid can subsequently be cleaved with *XhoI* and *HindIII* and ligated with the about 8 kbp *XhoI-HindIII* fragment of pUR4174, resulting in pUR4178 (see
25 Figure 6).

In the situation where pUR4175 was used as a starting vector, the resulting plasmid was designated pUR4179 (see Figure 7).

Both plasmids, pUR4178 and pUR4179 were introduced into *S. cerevisiae*.

Example 3. The modification of the binding parts of the chimeric protein that can bind traseolide® in order to improve the binding or release of traseolide® under certain conditions.

Modification of binding properties of antibodies during the immune response is a well known immunological phenomenon originating from the fine tuning of complementarity determining sequences in the antibody's binding region to the antigen's molecular properties. This phenomenon can be mimicked *in vitro* by adjusting the antigen binding regions of antibody fragments based on molecular models of these regions in contact with the antigen.

One such example consists of protein engineering the antimusk antibody M02/01/01 to a stronger binding variant M020501i.

First, a molecular model of M02/01/01 variable fragment (Fv) was constructed by homology modelling, using the coordinates of the anti-lysozyme antibody HYHEL-10 as a template (Brookhaven Protein Data Bank entry: 3HFM). This model was refined using Molecular Mechanics and Molecular Dynamics methods from within the Biosym program DISCOVER, on a Silicon Graphics 4D240 workstation.

Secondly, the binding site of the resulting Fv was mapped by visually docking the musk antigen into the CDR region, followed by a refinement using molecular dynamics again. Upon inspection of the resulting model for packing efficiency (van der Waals contact areas), it was concluded that substitution of ALA H96 by VAL would increase the (hydrophobic) contact area between the ligand and Fv, and consequently lead to a stronger interaction (see Figure 8).

When this mutation is introduced into M02/01/01, the cDNA-derived scFv from Example 2, the result will be Fv M020501i; a variant with an increased affinity of at least a factor of 5 can be expected, and the increased affinity could be measured using fluorescence titration of the Fv with the musk odour molecule.

Example 4. Construction of a gene encoding a chimeric protein that will be anchored in the cell wall of lower eukaryote and is able to bind hormones such as HCG.

Gene fragments, encoding the variable regions of the heavy and light chain fragments from the monoclonal antibody directed against the human chorionic gonadotropin were obtained from a hybridoma cell line in a similar way as described in Example 2.

Subsequently, these HCG V_H and V_L gene fragments were cloned into plasmid pUR4143 by replacing the corresponding *Pst*I-*Bst*EII and *Sac*I-*Xho*I gene fragments, resulting in plasmid pUR4146.

Similar to the method described in Example 2, the 734 bp *Eag*I-*Xho*I fragment (nucleotide sequence given in SEQ ID NO: 13) encoding the variable regions of the heavy and light chain fragments from the monoclonal antibody directed against the human chorionic gonadotropin (an scFv-HCG fragment) was isolated from pUR4146 and was introduced into the vector backbone fragment of pUR4178 (see Example 2) and will be introduced into the vector backbone fragment of pUR4175 (see Example 1), both digested with the same restriction enzymes. The resulting plasmids pUR4177 (see Figure 9) was, and pUR4180 (see Figure 10) will be, introduced into *S. cerevisiae* strain SU10.

20

Example 5. Construction of a gene encoding a chimeric scFv-FLO1 protein that will be anchored in the cell wall of lower eukaryote and is able to bind hormones such as HCG.

One of the genes associated with the flocculation phenotype in *S. cerevisiae* is the FLO1 gene. The DNA sequence of a clone containing major parts of the FLO1 gene has been determined, see SEQ ID NO: 14 giving 2685 bp of the FLO1 gene. The cloned fragment appeared to be approximately 2 kb shorter than the genomic copy as judged from Southern and Northern hybridizations, but encloses both ends of the FLO1 gene. Analysis of the DNA sequence data indicates that the putative protein contains at the N-terminus a hydrophobic region which confirms a signal sequence for secretion, a hydrophobic C-terminus that might function as a signal for the

30

attachment of a GPI-anchor and many glycosylation sites, especially in the C-terminus, with 46.6% serine and threonine in the arbitrarily defined C-terminus (aa 271-894). Hence, it is likely that the FLO1 gene product is located in an orientated fashion in the yeast cell wall and may be directly involved in the process
5 of interaction with neighbouring cells.

The cloned FLO1 sequence might therefore be suitable for the immobilization of proteins or peptides on the cell surface by a different type of cell wall anchor.

For the production of a chimeric protein comprising the scFv-HCG followed by the C-terminal part of the FLO1-protein, plasmid pUR2990 (see Figure 11) can be used
10 as a starting vector. The preparation of episomal plasmid pUR2990 was described in our co-pending patent application WO-94/01567 (UNILEVER) published on 20 January 1994, i.e. during the priority year. Plasmid pUR2990 comprises the chimeric gene consisting of the gene encoding the *Hunicola* lipase and a gene encoding the putative C-terminal cell wall anchor domain of the FLO1 gene product, the chimeric
15 gene being preceded by the invertase signal sequence (SUC2) and the GAL7 promoter; further the plasmid comprises the yeast 2 μ m sequence, the defective Leu2 promoter described by Eckard and Hollenberg (1983), and the Leu2 gene, see Roy c.s. (1991). Plasmid pUR4146, described in Example 4, can be digested with *Pst*I and *Xho*I, and the about 0.7 kbp *Pst*I-*Xho*I fragment containing the scFv-HCG
20 coding sequence can be isolated. For the in frame fusion of this DNA sequence between the C-terminal FLO1 part and the SUC2 signal sequence, the fragment can be directly ligated with the 9.3 kbp *Eag*I/*Nhe*I (partial) backbone of plasmid pUR2990, resulting in plasmid pUR4196 (see Figure 12). This plasmid will comprise an additional triplet encoding Ala at the transition between the SUC2 signal
25 sequence and the start of the scFv-HCG, and a E-I-K-G-G amino acid sequence in front of the first amino acid (Ser) of the C part of FLO1 protein.

If in the previous Examples 1-5 the level of exposed antibody fragments is too low, the production level can be increased by mutagenesis of the frame work regions of
30 the antibody fragment. This can be done in a site directed way or by (targeted) random mutagenesis, using techniques described in the literature.

Example 6. Construction of a gene encoding a chimeric protein that will be anchored in the cell wall of a lower eukaryote and is able to bind cholesterol.

In the literature two DNA sequences for cholesterol oxidase are described, the *choB* gene from *Brevibacterium sterolicum*, see Ohta c.s. (1991) and the *choA* gene from *Streptomyces* sp. SA-COO, see Ishizaka c.s. (1989). For the construction of a DNA fusion between the *choB* gene coding for cholesterol oxidase (EC 1.1.3.6) and the 3' part of the AG- α 1 gene, the PCR technique on chromosomal DNA can be applied. Chromosomal DNA can be isolated by standard techniques from *Brevibacterium sterolicum*, and the DNA part coding for the mature part of the cholesterol oxidase can be amplified through application with the following corresponding PCR primers cho01pcr and cho02pcr:

cho01pcr

15	5'-	GCC CCC AGC CGC ACC CTC G-3'	= SEQ ID NO: 16
	3'-	CGG GGG TCG GCG TGG GAG C-5'	= SEQ ID NO: 17
	5'-AGATCTGAATTCGGGCC	GCC CCC AGC CGC ACC CTC G-3'	= SEQ ID NO: 18
20		<div style="display: flex; justify-content: space-around; width: 100%;"> EcoRI NotI EagI </div>	

cho02pcr

		<div style="display: flex; justify-content: space-around; width: 100%;"> NheI HindIII </div>	
25	3'-TAG TAG AGC AGG CTG TAG GTC	<u>CGATCGACTTTCGAATCTAGA</u> -5'	= SEQ ID NO: 19
	5'-ATC ATC TCG TCC GAC ATC CAG-3'		= SEQ ID NO: 20
	3'-TAG TAG AGC AGG CTG TAG GTC-5'		= SEQ ID NO: 21

Both primers can specifically hybridize with the target sequence, thereby amplifying the coding part of the gene in such a way, that the specific PCR product -after Proteinase K treatment and digestion with *EcoRI* and *HindIII*- can be directly cloned into a suitable vector, here preferably pTZ19R, see Mead c.s. (1986). This will result in plasmid pUR2985 (see Figure 13).

In addition to the already mentioned restriction sites both PCR primers generate other restriction sites at the 5' end and the 3' end of the 1.5 kbp DNA fragment, which can be used later on to fuse the fragment in frame between either the SUC2 signal sequence or the prepro- α -mating factor signal sequence on one side and the C-terminus coding part of the α -agglutinin gene on the other side. To facilitate the ligation behind the prepro-MF sequence a *NorI* site is introduced at the 5' end of

PCR oligonucleotide cho01pcr, allowing for example, the exchange of the 731 bp *EagI/NheI* fragment containing the scFv-Lys coding sequence in pUR4175 for the *choB* coding sequence.

To create an enzymatically inactive fusion protein between cholesterol oxidase and α -agglutinin, the above described subcloning into pTZ19R can be used. Cholesterol oxidase is an FAD-dependent enzyme for which the crystal structure of the *Brevibacterium sterolicum* enzyme has been determined, see Vrielink c.s. (1991). The enzyme displays homology with the typical pattern of the FAD-binding domain with the Gly-X-Gly-X-X-Gly sequence near the N-terminus (amino acid 18-23). Site-directed *in vitro* mutagenesis on the plasmid pUR2985 according to the manufacturer's protocol (Muta-Gene kit, Bio-Rad) can be applied to inactivate the FAD-binding site through replacing the triplet(s) encoding the Gly residue(s) by triplets encoding other amino acids, thereby presumably inactivating the enzyme. E.g. the following primer can be used for site-directed mutagenesis of 2 of the conserved Gly residues.

pr	3'-	CGG	GAG	CAG	TAG	CGG	TCA	CGT	ATG	CCG	CCA	CGG	CAG	CGG	CGC	-5'
cs	5'-	GCC	CTC	GTC	ATC	GGC	AGT	GGA	TAC	GGC	GGT	GCC	GTC	GCC	GCG	-3'
		Ala				Gly		Gly		Gly	Gly	Ala		Ala	Ala	
						↓		↓								
						Ala		Ala								

pr = primer = SEQ ID NO: 22
cs = coding strand = SEQ ID NO: 23

As a result of the mutagenesis with the described primer, plasmid pUR2986 will be obtained. From this plasmid the DNA coding for the presumably inactivated cholesterol oxidase can be released as a 1527 bp fragment through *NotI/NheI* digestion, and subsequently directly used to exchange the scFv-Lys coding sequence in pUR4175, thereby generating plasmid pUR2987 (see Figure 14). To obtain a variant yeast secretion vector, where the secretion is directed through the SUC2 signal sequence, for example the 1823 bp long *SacI/NheI* segment of plasmid pUR2986 can be used to replace the *SacI/NheI* fragment in pUR4174.

This inactivation of the FAD-binding site might be preferable over other mutations, since an unchanged active centre can be expected to leave the binding properties of cholesterol oxidase for cholesterol unaltered. Instead of the described Gly-Ala

To inactivate the enzyme, site directed mutagenesis can be optionally immediately performed in the active site cavity, for example through exchange of the Glu331, a residue appropriately positioned to act as the proton acceptor, thus generating a new variant of an immobilized, enzymatically inactive fusion protein.

It has been described that proteinase of *Lactococcus lactis* subsp. *cremoris* is anchored to the cell wall through its 127 amino acid long C-terminal, see Kok c.s. (1988) and Kok (1990). In a way similar to that described in Example 6, the cholesterol oxidase of *Brevibacterium sterolicum* (*choB*) can be immobilized on the surface of *Lactococcus lactis*. Fusions can be made between the *choB* structural gene and the N-terminal signal sequence and the C-terminal anchor of the proteinase of *Lactococcus lactis*. Plasmid pGKV550 (see Figure 15) contains the complete proteinase operon of *Lactococcus lactis* subsp. *cremoris* Wg2, including the promoter, a ribosome binding site and DNA fragments encoding the already mentioned signal and anchor sequences, see Kok (1990). First a DNA fragment, containing the main part of the signal sequence, flanked by a *Cla*I site and an *Eag*I site can be constructed with PCR on pGKV550 as follows:

25 Primer prt1:
5'-AA GAT CTA TCG ATC TTG TTA GCC GGT ACA-3' = SEQ ID NO: 24
Proteinase gene (non coding strand):
3'-TT CCC GAT AGC TAG AAC AAT CGG CCA TGT CAG-5'
ClaI = SEQ ID NO: 25
30
Proteinase gene: Gln Ala Lys
5'-GTC GGC GAA ATC CAA GCA AAG GCG GCT-3' = SEQ ID NO: 26
Primer prt2: = SEQ ID NO: 27
3'-CAG CCG CTT TAG GTT CGT TGC CGG CCC CCC TTC GAA CCC-5'
35 EaqI HindIII

After the PCR reaction as described in Example 6, the 98 bp long PCR fragment can be isolated and digested with *ClaI* and *HindIII*. pGKV550 can subsequently be cleaved partially with *ClaI* and completely with *HindIII*, after which digestions the vector fragment, containing the promoter, the ribosome binding site, the DNA
 5 fragment encoding the N-terminal 8 amino acids and the cell wall binding fragment containing the 127 C-terminal amino acids of the proteinase gene can be isolated on gel.

A copy of the cholesterol oxidase gene, suitable for fusion with the prtP anchor domain can be produced by a PCR reaction using plasmid pUR2985 (Example 6) as
 10 template and a combination of primer cho01pcr (see Example 6) and the following primer cho03pcr instead of primer cho02pcr:

	cho03pcr		<i>HindIII</i>	
	3'-TAG TAG AGC AGG CTG TAG GTC CGA		<u>GTT CGA</u> ACC TAG GC-5'	= SEQ ID NO: 40
15				
	5'-ATC ATC TCG TCC GAC ATC CAG			= SEQ ID NO: 20.

The about 1.53 kbp fragment generated by this reaction can be digested with *NotI* and *HindIII* to produce a molecule which can subsequently be ligated with the large *EagI/HindIII* fragment from pUR2988 (see Figure 16). The resulting plasmid,
 20 pUR2989, will contain the cholesterol oxidase coding sequence inserted between the signal sequence and the C-terminal cell wall anchor domain of the proteinase gene. After introduction into *Lactobacillus lactis* subsp. *lactis* MG1363 by electroporation, this plasmid will express cholesterol oxidase under control of the proteinase promoter. The transport through the membrane will be mediated by the proteinase
 25 signal sequence and the immobilization of the cholesterol oxidase by the proteinase anchor. As it is unlikely that the *Lactococcus* will secrete FAD as well, the cholesterol oxidase will not be active but will be capable to bind cholesterol.

30 Example 8. Construction of a gene encoding a chimeric protein that will be anchored in the cell wall of a lower eukaryote and is able to bind growth hormones, such as the epidermal growth factor.

For the isolation of larger amounts of human epidermal growth factor (EGF) the corresponding receptor can be used in form of a fusion between the binding domain

and a C-terminal part of α -agglutinin as cell wall anchor. The complete cDNA sequence of the human epidermal growth factor is cloned and sequenced. For the construction of a fusion protein with EGF binding capacity the N-terminal part of the mature receptor until the central 23 amino acids transmembrane region can be
5 utilized.

The plasmid pUR4175 can be used for the construction. Through digestion with *EagI* and *NheI* (partial) a 731 bp DNA fragment containing the sequence coding for scFv is released and can be replaced by a DNA fragment coding for the first 621 amino acids of human epidermal growth factor receptor. Initiating from an existing
10 human cDNA library or otherwise through production of a cDNA library by standard techniques from preferentially EGF receptor overexpressing cells, e.g. A431 carcinoma cells, see Ullrich c.s. (1984), further PCR can be applied for the generation of in frame linkage between the extracellular binding domain of the human growth factor receptor (amino acid 1-622) and the C-terminal part of
15 α -agglutinin.

PCR oligonucleotides for the in frame linkage of human epidermal growth factor receptor and the C-terminus of α -agglutinin.

- 20 a: PCR oligonucleotides for the transition between SUC2 signal sequence and the N-terminus of mature EGF receptor.

		> mature EGF receptor										
	pri EGF1:	Ala	Leu	Glu	Lys	Lys	Val					= SEQ ID NO: 28
	5'-GGG	GCG	GCC	GCG	CTG	GAG	GAA	AAG	AAA	GTT	TGC	-3'
25		NotI										
	3'-CGC	TCA	GEC	CGA	GAC	CTC	CTT	TTC	TTT	CAA	ACG	5'
	EGF rec (non-coding strand):											= SEQ ID NO: 29

- b: PCR oligonucleotides for the in frame transition between C terminus of the
30 extracellular binding domain of EGF receptor and the C terminal part of α -agglutinin.

EGF rec (coding strand):

	Asn	Gly	Pro		Ile	Pro	Ser		Ala	Thr	
5'	-AAT	GGG	CCT	AAG	ATC	CCG	TCC	ATC	GCC	ACT	-3'
5	3'	-TTA	CCC	GGA	TTC	TAG	GGC	AGG	<u>CGA</u>	<u>TCGGAATT</u>	<u>TCGAA</u>
	pr EGF2:								<u>NheI</u>	<u>HindIII</u>	CCCC-5'

This fusion would result in an addition of 2 Ala amino acids between the signal sequence and the mature N-terminus of EGF receptor.

The newly obtained 1.9 kbp PCR fragment can be digested with *NotI* and *NheI* and directly ligated into the vector pUR4175 after digesting with the same enzymes, resulting in plasmid pUR2993 (see Figure 17), comprising the GAL7 promoter, the prepro- α -mating factor sequence, the chimeric EGF receptor binding domain gene / α -agglutinin gene, the yeast 2 μ m sequence, the defective LEU2 promoter and the LEU2 gene. This plasmid can be transformed into *S. cerevisiae* and the transformed cells can be cultivated in YP medium whereby expression of the chimeric protein can be induced by adding galactose to the medium.

Example 9. Construction of genes encoding a chimeric protein anchored to the cell wall of yeast, comprising a binding domain of a "Camelidae" heavy chain antibody

Recently it was described that camels as well as a number of related species (e.g. llamas) contain a considerable amount of IgG antibody molecules which are only composed of heavy-chain dimers, see Hamers-Casterman c.s. (1993). Although these "heavy-chain" antibodies are devoid of light chains, it was demonstrated, that they nevertheless have an extensive antigen-binding repertoire. In order to show that the variable regions of this type of antibodies can be produced and will be linked to the exterior of the cell wall of a yeast, the following constructs were prepared.

30 Construction of pUR2997, pUR2998 and pUR2999

The about 2.1 kbp *EagI*-*HindIII* fragment of pUR4177 (Example 4, Fig 9) was isolated. By using PCR technology, an *EcoRI* restriction site was introduced immediately upstream of the *EagI* site, whereby the C of the *EcoRI* site is the same as the first C of the *EagI* site. The thus obtained *EcoRI*-*HindIII* fragment was

ligated into plasmid pEMBL9, which was digested with *EcoRI* and *HindIII*, which resulted in pUR4177.A

The *EcoRI/NheI* fragment of plasmid pUR4177.A was replaced by the *EcoRI/NheI* fragments of three different synthetic DNA fragments (SEQ ID NO: 32, SEQ ID NO: 33, and SEQ ID NO: 34) resulting in pUR2997, pUR2998 and pUR2999, respectively. The about 1.5 kbp *BstEII-HindIII* fragments of pUR2997 and pUR2998 were isolated.

Construction of pUR4421

10 The multiple cloning site of plasmid pEMBL9, see Dente c.s. (1983), (ranging from the *EcoRI* to the *HindIII* site) was replaced by a synthetic DNA fragment having the nucleotide sequence given below, see SEQ ID NO: 35 giving the coding strand and SEQ ID NO: 36 giving the non-coding strand. The 5'-part of this nucleotide sequence comprises an *EagI* site, the first 4 codons of a *Camelidae* V_H gene
15 fragment (nucleotides 16-27) and a *XhoI* site (CTCGAG) coinciding with codons 5 and 6 (nucleotides 28-33). The 3'-part comprises the last 5 codons of the *Camelidae* V_H gene (nucleotides 46-60) (part of which coincides with a *BstEII* site), eleven codons of the Myc tail (nucleotides 61-93), see SEQ ID NO: 35 containing these eleven codons and SEQ ID NO: 37 giving the amino acid sequence, and an *EcoRI*
20 site (GAATTC). The *EcoRI* site, originally present in pEMBL9, is not functional any more, because the 5'- end of the nucleotide sequence contains AATTT instead of AATTC, indicated below as (*EcoRI*). The resulting plasmid is called pUR4421. The *Camelidae* V_H fragment starts with amino acids Q-V-K and ends with amino acids V-S-S.

25	(<i>EcoRI</i>)	<i>EagI</i>		<i>XhoI</i>		<i>BstEII</i>	
	5'-	<u>AATTTAGCGG</u>	<u>CCGCCCAGGT</u>	<u>GAAACTGCTC</u>	<u>GAGTAAGTGA</u>	<u>CTAAGGTCAC</u>	- 50
	3' 1	ATCGCC	GGCGGGTCCA	CTTTGACGAG	CTCATTCACT	GATTCCAGTG-	
		5	Q V K				
30		-CGTCTCCTCA	GAACAAAAAC	TCATCTCAGA	AGAGGATCTG	AATTAATGAG-	100
		-GCAGAGGAGT	CTTGTTTTTG	AGTAGAGTCT	TCTCCTAGAC	TTAATTACTC-	
		V S S	E Q K	L I S E	E D L	N * *	
						= SEQ ID NO: 37	
35	<i>EcoRI</i>		<i>HindIII</i>				
	-	<u>AATTCATCAA</u>	<u>ACGGTGATA</u>	-3'	119	= SEQ ID NO: 35	
	-	TTAAGTAGTT	TGCCACTATT CGA	-5'	123	= SEQ ID NO: 36	

Construction of pUR4424

After digesting the plasmid pB09 with *Xho*I and *Bst*EII, a DNA fragment of about 0.34 kbp was isolated from agarose gel. This fragment codes for a truncated V_H fragment, missing both the first 4 and the last 5 amino acids of the *Camelidae* V_H fragment. Plasmid pB09 was deposited as *E. coli* JM109 pB09 at the Centraal Bureau voor Schimmelcultures, Baarn on 20 April 1993 with deposition number CBS 271.93. The DNA and amino acid sequences of the Camel V_H fragments followed by the Flag sequence as present in plasmid pB09 were given in Figure 6B of European patent application 93201239.6 (not yet published), which is herein incorporated by reference. The obtained about 0.34 kbp fragment was cloned into pUR4421. To this end plasmid pUR4421 was digested with *Xho*I and *Hind*III, after which the about 4 kb vector fragment was isolated from an agarose gel. The resulting vector was ligated with the about 0.34 kbp *Xho*I/*Bst*EII fragment and a synthetic DNA linker having the following sequence:

15	<div style="display: inline-block; text-align: left; width: 40%;"> <i>Bst</i>EII </div> <div style="display: inline-block; text-align: right; width: 40%;"> <i>Hind</i>III </div>	
	<div style="border-bottom: 1px solid black; display: inline-block;"> GTCACCGTCTCCTCATAATGA </div>	= SEQ ID NO: 38
	GCAGAGGAGTATTACTTCGA	= SEQ ID NO: 39

resulting in plasmid pUR4421-09.

20 Plasmid pSY16 was digested with *Eag*I and *Hind*III, after which the about 6.5 kbp long vector backbone was isolated and ligated with the about 0.38 kbp *Eag*I/*Hind*III fragment from pUR4421-09 resulting in pUR4424.

Construction of pUR4482 and pUR4483

25 From pUR4424 the about 0.44 kbp *Sac*I-*Bst*EII fragment, coding for the invertase signal sequence and the camel heavy chain variable 09 (= CH_V09) fragment, was isolated as well as the about 6.3 kbp *Sac*I-*Hind*III vector fragment. The about 6.3 kbp fragment and the about 0.44 kbp fragment from pUR4424 were ligated with the *Bst*EII-*Hind*III fragment from pUR2997 or pUR2998 yielding pUR4482 and

30 pUR4483, respectively.

Plasmid pUR4482 is thus an yeast episomal expression plasmid for expression of a fusion protein with the invertase signal sequence, the CH_V09 variable region, the Myc-tail and the Camel "X-P-X-P" Hinge region, see Hamers-Casterman c.s. (1993),

(1993), and the α -agglutinin cell wall anchor region. Plasmid pUR4483 differs from pUR4482 in that it contains the Myc-tail but not the "X-P-X-P" Hinge region.

Similarly, the *Bst*EII-*Hind*III fragment from pUR2999 can be ligated with the about 6.3 kbp vector fragment and the about 0.44 kbp fragment from pUR4424, resulting
 5 in pUR4497, which will differ from pUR4482 in that it contains the "X-P-X-P" Hinge region but not the Myc-tail.

The plasmids pUR4424, pUR4482 and pUR4483 were introduced into *Saccharomyces cerevisiae* SU10 by electroporation, and transformants were selected on plates lacking leucine. Transformants from SU10 with pUR4424, pUR4482 or
 10 pUR4483, respectively, were grown on YP with 5% galactose and analysed with immuno-fluorescence microscopy, as described in Example 1 of our co-pending WO-94/01567 (UNILEVER) published on 20 January 1994. This method was slightly modified to detect the chimeric proteins, containing both the camel antibody and the Myc tail, present at the cell surface.

15 In one method a monoclonal mouse anti-Myc antibody was used as a first antibody to bind to the Myc part of the chimeric protein; subsequently a polyclonal anti-mouse Ig antiserum labeled with fluorescein isothiocyanate (= FITC) ex Sigma, Product No. F-0527, was used to detect the bound mouse antibody and a positive signal was determined by fluorescence microscopy.

20 In the other method a polyclonal rabbit anti-human IgG serum, which had earlier been proven to cross-react with the camel antibodies, was used as a first antibody to bind the camel antibody part of the chimeric protein; subsequently a polyclonal anti-rabbit Ig antiserum labeled with FITC ex Sigma, Product No. F-0382, was used to detect the bound rabbit antibody and a positive signal was determined by
 25 fluorescence microscopy.

The results in Figure 19 and Figure 20 show clearly that fluorescence can be observed on those cells in which a fusion protein of the CH_v09 fragment with the α -agglutinin cell wall anchor region is produced (pUR4482 and pUR4483). No
 30 fluorescence however, was visible on the cells which produce the CH_v09 fragment without this anchor (pUR4424), when viewed under the same circumstances.

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- 5 WO-91/00920 (UNILEVER) Process for preparing a protein by a fungus transformed by multicopy integration of an expression vector. First priority date 07.07.89; published 24.01.91
- WO-91/19782 (UNILEVER) Xylanase production. Priority date 19.06.90; published 26.12.91
- 10 WO-94/01567 (UNILEVER) Process for immobilizing enzymes to the cell wall of a microbial cell by producing a fusion protein. First priority date 08.07.92; published 20.01.94
- EP patent application 93201239.6 (not yet published) Production of antibodies or (functionalized) fragments thereof derived from heavy chain immunoglobulins of
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25

Information on a deposit of a micro-organism under the Budapest Treaty is given on page 26, lines 5-7 above . In agreement with Rule 28 (4) EPC, or a similar arrangement for a State not being a Contracting State of the EPC, it is hereby requested that a sample of such deposit, when requested, will be submitted to an

30 expert only.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(B) STREET: Hagedoorn 18
(C) CITY: Maassluis
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): NL-3142 KB

(ii) TITLE OF INVENTION: Immobilized proteins with specific binding capacities and their use in processes and products.

(iii) NUMBER OF SEQUENCES: 40

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: fragment in pUR4119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCGAGC TCATCACACA AACAAACAAA ACAAATGAT GCTTTTGCAA GCCTTTCTTT 60
 TCCTTTTGGC TGGTTTTCGA GCCAAAATAT CTGCGCAGGT GCAGCTGCAG TAATGAACCA 120
 CGGTCACCGT CTCCTCAGGT GGAGGCGGTT CAGGCGGAGG TGGCTCTGGC GGTGGCGGAT 180
 CGGACATCGA GCTCACTCAG ACCAAGCTCG AGATCAAACG GTGATAAGCT T 231

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker XhoI-NheI coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCGAGATCAA AGGCGGATCT G 21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker XhoI-NheI non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTAGCAGATC CGCCTTTGAT C 21

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker EagI-PstI coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCCGCCAG GTGCAGCTGC A 21

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: linker EagI-PstI non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTGCACCTG GGC

13

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PCR primer A (heavy chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGTSMARCT GCAGSAGTCW GG

22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PCR primer B (heavy chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGAGGAGACG GTGACCGTGG TCCCTTGGCC CC

32

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PCR primer C (light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GACATTGAGC TCACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PCR primer D (light chain)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTTTGATCTC GAGCTTGGTC CC

22

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: linker EcoRI-PstI coding strand

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AATTCGGCCG TTCAGGTGCA GCTGCA

26

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: linker EcoRI-PstI non-coding strand

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCTGCACCTG AACGGCCG

18

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ScFv antitraxolide 02/01/01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTGCAGGAGT CTGGACCTGG CCTGGTGAAA CTTTCTCAGT CTCTGTCCCT CACCTGCACT	60
GTCAGTGGCT ACTCAATCAC CAGTGATTTT GCCTGGAACT GGATCCGGCA GTTTCAGGA	120
AACCAACTGG AGTGGATGGG CTACATAAGC TACAGTGGTA GCACTAGCTA CAACCCATCT	180
CTCAAAGTC GAATCTCTCT CACTCGAGAC ACATCCAAGA ACCAGTTCTT CCTGCAGTTG	240
AATTCTGTGA CTACTGAGGA CACAGCCACA TATTACTGTG CAACGTCCCT AACATGGTTA	300
CTACGTCGGA AACGTTCTTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCAGGTGGA	360
GGCGGTTTCA GCGGAGGTGG CTCTGGCGGT GCGGATCGG ACATCGAGCT CACCCAGTCT	420
CCATCCTCCA TGTCTGTATC TCTGGGAGAC ACAGTCAGCA TCACTTGCCA TGCAAGTCAG	480
GACATTAGCA GTAATATAGG GTGGTTGCAG CAGAAACCAG GGAAATCATT TAAGGGCCTG	540
ATCTATCATG GAACCAACTT GGAAGATGGT ATTCCATCAA GGTTCACTGG CAGTGGATCT	600
GGAGCAGATT ATTCCCTCAC CATCAGCAGC CTGGAATCTG AAGATTTTGC AGACTATTAC	660
TGTGTACAGT ATGCTCAGTT TCCATTACAG TTCGGCTCGG GGACCAAGCT CGAG	714

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ScFv anti-HCG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGCCGTTCA GGTGCAGCTG CAGGAGTCTG GGGGACACTT AGTGAAGCCT GGAGGGTCCC	60
TGAAACTCTC CTGTGCAGCC TCTGGATTCT CTTTCAGTAG CTTTGACATG TCTTGGATTG	120
GCCAGACTCC GGAGAAGAGG CTGGAGTGGG TCGCAAGCAT TACTAATGTT GGTACTTACA	180
CCTACTATCC AGGCAGTGTG AAGGGCCGAT TCTCCATCTC CAGAGACAAT GCCAGGAACA	240
CCCTAAACCT GCAAATGAGC AGTCTGAGGT CTGAGGACAC GGCCTTGTAT TTCTGTGCAA	300
GACAGGGGAC TCGGGCACAA CCTTACTGGT ACTTCGATGT CTGGGGCCAA GGGACCACGG	360
TCACCGTCTC CTCAGGTGGA GCGGTTTCA GCGGAGGTGG CTCTGGCGGT GCGGATCGG	420
ACATCGAGCT CACCCAGTCT CCAAATCCA TGTCCATGTC CGTAGGAGAG AGGGTCACCT	480
TGAGCTGCAA GGCCAGTGAG ACTGTGGATT CTTTGTGTG CTGGTATCAA CAGAAACCAG	540
AACAGTCTCC TAAATTGTTG ATATTCGGGG CATCCAACCG GTTCAGTGGG GTCCCCGATC	600
GCTTCACTGG CAGTGGATCT GCAACAGACT TCACTCTGAC CATCAGCAGT GTGCAGGCTG	660
AGGACTTTGC GGATTACCAC TGTGGACAGA CTTACAATCA TCCGTATACG TTCGGAGGGG	720
GGACCAAGCT CGAG	734

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pYY105

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2685
- (D) OTHER INFORMATION: /product= "Flocculation protein"
/gene= "FLO1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATG ACA ATG CCT CAT CGC TAT ATG TTT TTG GCA GTC TTT ACA CTT CTG	48
Met Thr Met Pro His Arg Tyr Met Phe Leu Ala Val Phe Thr Leu Leu	
1 5 10 15	
GCA CTA ACT AGT GTG GCC TCA GGA GCC ACA GAG GCG TGC TTA CCA GCA	96
Ala Leu Thr Ser Val Ala Ser Gly Ala Thr Glu Ala Cys Leu Pro Ala	
20 25 30	
GGC CAG AGG AAA ACT GGG ATG AAT ATA AAT TTT TAC CAG TAT TCA TTG	144
Gly Gln Arg Lys Ser Gly Met Asn Ile Asn Phe Tyr Gln Tyr Ser Leu	
35 40 45	
AAA GAT TCC TCC ACA TAT TCG AAT GCA GCA TAT ATG GCT TAT GGA TAT	192
Lys Asp Ser Ser Thr Tyr Ser Asn Ala Ala Tyr Met Ala Tyr Gly Tyr	
50 55 60	
GCC TCA AAA ACC AAA CTA GGT TCT GTC GGA GGA CAA ACT GAT ATC TCG	240
Ala Ser Lys Thr Lys Leu Gly Ser Val Gly Gly Gln Thr Asp Ile Ser	
65 70 75 80	
ATT GAT TAT AAT ATT CCC TGT GTT AGT TCA TCA GGC ACA TTT CCT TGT	288
Ile Asp Tyr Asn Ile Pro Cys Val Ser Ser Ser Gly Thr Phe Pro Cys	
85 90 95	
CCT CAA GAA GAT TCC TAT GGA AAC TGG GGA TGC AAA GGA ATG GGT GCT	336
Pro Gln Glu Asp Ser Tyr Gly Asn Trp Gly Cys Lys Gly Met Gly Ala	
100 105 110	
TGT TCT AAT AGT CAA GGA ATT GCA TAC TGG AGT ACT GAT TTA TTT GGT	384
Cys Ser Asn Ser Gln Gly Ile Ala Tyr Trp Ser Thr Asp Leu Phe Gly	
115 120 125	
TTC TAT ACT ACC CCA ACA AAC GTA ACC CTA GAA ATG ACA GGT TAT TTT	432
Phe Tyr Thr Thr Pro Thr Asn Val Thr Leu Glu Met Thr Gly Tyr Phe	
130 135 140	
TTA CCA CCA CAG ACG GGT TCT TAC ACA TTC AAG TTT GCT ACA GTT GAC	480
Leu Pro Pro Gln Thr Gly Ser Tyr Thr Phe Lys Phe Ala Thr Val Asp	
145 150 155 160	
GAC TCT GCA ATT CTA TCA GTA GGT GGT GCA ACC GCG TTC AAC TGT TGT	528
Asp Ser Ala Ile Leu Ser Val Gly Gly Ala Thr Ala Phe Asn Cys Cys	
165 170 175	

GCT	CAA	CAG	CAA	CCG	CCG	ATC	ACA	TCA	ACG	AAC	TTT	ACC	ATT	GAC	GGT	576
Ala	Gln	Gln	Gln	Pro	Pro	Ile	Thr	Ser	Thr	Asn	Phe	Thr	Ile	Asp	Gly	
			180					185					190			
ATC	AAG	CCA	TGG	GGT	GGA	AGT	TTG	CCA	CCT	AAT	ATC	GAA	GGA	ACC	GTC	624
Ile	Lys	Pro	Trp	Gly	Gly	Ser	Leu	Pro	Pro	Asn	Ile	Glu	Gly	Thr	Val	
		195					200					205				
TAT	ATG	TAC	GCT	GGC	TAC	TAT	TAT	CCA	ATG	AAG	GTT	GTT	TAC	TCG	AAC	672
Tyr	Met	Tyr	Ala	Gly	Tyr	Tyr	Tyr	Pro	Met	Lys	Val	Val	Tyr	Ser	Asn	
	210					215					220					
GCT	GTT	TCT	TGG	GGT	ACA	CTT	CCA	ATT	AGT	GTG	ACA	CTT	CCA	GAT	GGT	720
Ala	Val	Ser	Trp	Gly	Thr	Leu	Pro	Ile	Ser	Val	Thr	Leu	Pro	Asp	Gly	
225					230				235					240		
ACC	ACT	GTA	AGT	GAT	GAC	TTC	GAA	GGG	TAC	GTC	TAT	TCC	TTT	GAC	GAT	768
Thr	Thr	Val	Ser	Asp	Asp	Phe	Glu	Gly	Tyr	Val	Tyr	Ser	Phe	Asp	Asp	
			245						250					255		
GAC	CTA	AGT	CAA	TCT	AAC	TGT	ACT	GTC	CCT	GAC	CCT	TCA	AAT	TAT	GCT	816
Asp	Leu	Ser	Gln	Ser	Asn	Cys	Thr	Val	Pro	Asp	Pro	Ser	Asn	Tyr	Ala	
			260					265					270			
GTC	AGT	ACC	ACT	ACA	ACT	ACA	ACG	GAA	CCA	TGG	ACC	GGT	ACT	TTC	ACT	864
Val	Ser	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Pro	Trp	Thr	Gly	Thr	Phe	Thr	
		275					280					285				
TCT	ACA	TCT	ACT	GAA	ATG	ACC	ACC	GTC	ACC	GGT	ACC	AAC	GGC	GTT	CCA	912
Ser	Thr	Ser	Thr	Glu	Met	Thr	Thr	Val	Thr	Gly	Thr	Asn	Gly	Val	Pro	
	290					295					300					
ACT	GAC	GAA	ACC	GTC	ATT	GTC	ATC	AGA	ACT	CCA	ACC	AGT	GAA	GGT	CTA	960
Thr	Asp	Glu	Thr	Val	Ile	Val	Ile	Arg	Thr	Pro	Thr	Ser	Glu	Gly	Leu	
305					310				315					320		
ATC	AGC	ACC	ACC	ACT	GAA	CCA	TGG	ACT	GGC	ACT	TTC	ACT	TCG	ACT	TCC	1008
Ile	Ser	Thr	Thr	Thr	Glu	Pro	Trp	Thr	Gly	Thr	Phe	Thr	Ser	Thr	Ser	
				325					330					335		
ACT	GAG	GTT	ACC	ACC	ATC	ACT	GGA	ACC	AAC	GGT	CAA	CCA	ACT	GAC	GAA	1056
Thr	Glu	Val	Thr	Thr	Ile	Thr	Gly	Thr	Asn	Gly	Gln	Pro	Thr	Asp	Glu	
			340				345					350				
ACT	GTG	ATT	GTT	ATC	AGA	ACT	CCA	ACC	AGT	GAA	GGT	CTA	ATC	AGC	ACC	1104
Thr	Val	Ile	Val	Ile	Arg	Thr	Pro	Thr	Ser	Glu	Gly	Leu	Ile	Ser	Thr	
		355					360					365				
ACC	ACT	GAA	CCA	TGG	ACT	GGT	ACT	TTC	ACT	TCT	ACA	TCT	ACT	GAA	ATG	1152
Thr	Thr	Glu	Pro	Trp	Thr	Gly	Thr	Phe	Thr	Ser	Thr	Ser	Thr	Glu	Met	
		370				375					380					
ACC	ACC	GTC	ACC	GGT	ACT	AAC	GGT	CAA	CCA	ACT	GAC	GAA	ACC	GTG	ATT	1200
Thr	Thr	Val	Thr	Gly	Thr	Asn	Gly	Gln	Pro	Thr	Asp	Glu	Thr	Val	Ile	
385					390				395					400		
GTT	ATC	AGA	ACT	CCA	ACC	AGT	GAA	GGT	TTG	GTT	ACA	ACC	ACC	ACT	GAA	1248
Val	Ile	Arg	Thr	Pro	Thr	Ser	Glu	Gly	Leu	Val	Thr	Thr	Thr	Thr	Glu	
				405					410					415		
CCA	TGG	ACT	GGT	ACT	TTT	ACT	TCG	ACT	TCC	ACT	GAA	ATG	TCT	ACT	GTC	1296
Pro	Trp	Thr	Gly	Thr	Phe	Thr	Ser	Thr	Ser	Thr	Glu	Met	Ser	Thr	Val	
			420				425						430			
ACT	GGA	ACC	AAT	GGC	TTG	CCA	ACT	GAT	GAA	ACT	GTC	ATT	GTT	GTC	AAA	1344
Thr	Gly	Thr	Asn	Gly	Leu	Pro	Thr	Asp	Glu	Thr	Val	Ile	Val	Val	Lys	
		435					440					445				

ACT Thr 450	CCA Pro	ACT Thr	ACT Thr	GCC Ala	ATC Ile	TCA Ser 455	TCC Ser	AGT Ser	TTG Leu	TCA Ser 460	TCA Ser	TCA Ser	TCT Ser	TCA Ser	GGA Gly	1392
CAA Gln 465	ATC Ile	ACC Thr	AGC Ser	TCT Ser	ATC Ile 470	ACG Thr	TCT Ser	TCG Ser	CGT Arg	CCA Pro 475	ATT Ile	ATT Ile	ACC Thr	CCA Pro	TTC Phe 480	1440
TAT Tyr	CCT Pro	AGC Ser	AAT Asn	GGA Gly 485	ACT Thr	TCT Ser	GTG Val	ATT Ile	TCT Ser 490	TCC Ser	TCA Ser	GTA Val	ATT Ile	TCT Ser 495	TCC Ser	1488
TCA Ser	GTC Val	ACT Thr	TCT Ser	TCT Ser	CTA Leu	TTC Phe	ACT Thr	TCT Ser	TCT Ser	CCA Pro	GTC Val	ATT Ile	TCT Ser	TCC Ser	TCA Ser	1536
GTC Val	ATT Ile	TCT Ser 515	TCT Ser	TCT Ser	ACA Thr	ACA Thr	ACC Thr 520	TCC Ser	ACT Thr	TCT Ser	ATA Ile	TTT Phe 525	TCT Ser	GAA Glu	TCA Ser	1584
TCT Ser 530	AAA Lys	TCA Ser	TCC Ser	GTC Val	ATT Ile	CCA Pro 535	ACC Thr	AGT Ser	AGT Ser	TCC Ser	ACC Thr 540	TCT Ser	GGT Gly	TCT Ser	TCT Ser	1632
GAG Glu 545	AGC Ser	GAA Glu	ACG Thr	AGT Ser	TCA Ser 550	GCT Ala	GGT Gly	TCT Ser	GTC Val	TCT Ser 555	TCT Ser	TCC Ser	TCT Ser	TTT Phe	ATC Ile 560	1680
TCT Ser	TCT Ser	GAA Glu	TCA Ser	TCA Ser	AAA Lys 565	TCT Ser	CCT Pro	ACA Thr	TAT Tyr 570	TCT Ser	TCT Ser	TCA Ser	TCA Ser	TTA Leu 575	CCA Pro	1728
CTT Leu	GTT Val	ACC Thr	AGT Ser	GCG Ala	ACA Thr	ACA Thr	AGC Ser	CAG Gln	GAA Glu	ACT Thr	GCT Ala	TCT Ser	TCA Ser	TTA Leu	CCA Pro	1776
CCT Pro	GCT Ala	ACC Thr	ACT Thr	ACA Thr	AAA Lys	ACG Thr	AGC Ser	GAA Glu	CAA Gln	ACC Thr	ACT Thr	TTG Leu 605	GTT Val	ACC Thr	GTG Val	1824
ACA Thr 610	TCC Ser	TGC Cys	GAG Glu	TCT Ser	CAT His 615	GTG Val	TGC Cys	ACT Thr	GAA Glu	TCC Ser	ATC Ile 620	TCC Ser	CCT Pro	GCG Ala	ATT Ile	1872
GTT Val 625	TCC Ser	ACA Thr	GCT Ala	ACT Thr	GTT Val 630	ACT Thr	GTT Val	AGC Ser	GGC Gly	GTC Val 635	ACA Thr	ACA Thr	GAG Glu	TAT Tyr	ACC Thr 640	1920
ACA Thr	TGG Trp	TGC Cys	CCT Pro	ATT Ile 645	TCT Ser	ACT Thr	ACA Thr	GAG Glu	ACA Thr 650	ACA Thr	AAG Lys	CAA Gln	ACC Thr	AAA Lys	GGG Gly 655	1968
ACA Thr	ACA Thr	GAG Glu	CAA Gln 660	ACC Thr	ACA Thr	GAA Glu	ACA Thr	ACA Thr	AAA Lys	CAA Gln	ACC Thr	ACG Thr	GTA Val 670	GTT Val	ACA Thr	2016
ATT Ile	TCT Ser	TCT Ser	TGT Cys	GAA Glu	TCT Ser	GAC Asp	GTA Val 680	TGC Cys	TCT Ser	AAG Lys	ACT Thr	GCT Ala 685	TCT Ser	CCA Pro	GCC Ala	2064
ATT Ile 690	GTA Val	TCT Ser	ACA Thr	AGC Ser	ACT Thr	GCT Ala 695	ACT Thr	ATT Ile	AAC Asn	GGC Gly	GTT Val 700	ACT Thr	ACA Thr	GAA Glu	TAC Tyr	2112
ACA Thr 705	ACA Thr	TGG Trp	TGT Cys	CCT Pro	ATT Ile 710	TCC Ser	ACC Thr	ACA Thr	GAA Glu	TCG Ser 715	AGG Arg	CAA Gln	CAA Gln	ACA Thr	ACG Thr 720	2160

CTA GTT ACT GTT ACT TCC TGC GAA TCT GGT GTG TGT TCC GAA ACT GCT Leu Val Thr Val Thr Ser Cys Glu Ser Gly Val Cys Ser Glu Thr Ala 725 730 735	2208
TCA CCT GCC ATT GTT TCG ACG GCC ACG GCT ACT GTG AAT GAT GTT GTT Ser Pro Ala Ile Val Ser Thr Ala Thr Val Asn Asp Val Val 740 745 750	2256
ACG GTC TAT CCT ACA TGG AGG CCA CAG ACT GCG AAT GAA GAG TCT GTC Thr Val Tyr Pro Thr Trp Arg Pro Gln Thr Ala Asn Glu Glu Ser Val 755 760 765	2304
AGC TCT AAA ATG AAC AGT GCT ACC GGT GAG ACA ACA ACC AAT ACT TTA Ser Ser Lys Met Asn Ser Ala Thr Gly Glu Thr Thr Thr Asn Thr Leu 770 775 780	2352
GCT GCT GAA ACG ACT ACC AAT ACT GTA GCT GCT GAG ACG ATT ACC AAT Ala Ala Glu Thr Thr Thr Asn Thr Val Ala Ala Glu Thr Ile Thr Asn 785 790 795 800	2400
ACT GGA GCT GCT GAG ACG AAA ACA GTA GTC ACC TCT TCG CTT TCA AGA Thr Gly Ala Ala Glu Thr Lys Thr Val Val Thr Ser Ser Leu Ser Arg 805 810 815	2448
TCT AAT CAC GCT GAA ACA CAG ACG GCT TCC GCG ACC GAT GTG ATT GGT Ser Asn His Ala Glu Thr Gln Thr Ala Ser Ala Thr Asp Val Ile Gly 820 825 830	2496
CAC AGC AGT AGT GTT GTT TCT GTA TCC GAA ACT GGC AAC ACC AAG AGT His Ser Ser Ser Val Val Ser Val Ser Glu Thr Gly Asn Thr Lys Ser 835 840 845	2544
CTA ACA AGT TCC GGG TTG AGT ACT ATG TCG CAA CAG CCT CGT AGC ACA Leu Thr Ser Ser Gly Leu Ser Thr Met Ser Gln Gln Pro Arg Ser Thr 850 855 860	2592
CCA GCA AGC AGC ATG GTA GGA TAT AGT ACA GCT TCT TTA GAA ATT TCA Pro Ala Ser Ser Met Val Gly Tyr Ser Thr Ala Ser Leu Glu Ile Ser 865 870 875 880	2640
ACG TAT GCT GGC AGT GCA ACA GCT TAC TGG CCG GTA GTG GTT TAA Thr Tyr Ala Gly Ser Ala Thr Ala Tyr Trp Pro Val Val Val 885 890 895	2685

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 894 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Met Thr Met Pro His Arg Tyr Met Phe Leu Ala Val Phe Thr Leu Leu 1 5 10 15
Ala Leu Thr Ser Val Ala Ser Gly Ala Thr Glu Ala Cys Leu Pro Ala 20 25 30
Gly Gln Arg Lys Ser Gly Met Asn Ile Asn Phe Tyr Gln Tyr Ser Leu 35 40 45
Lys Asp Ser Ser Thr Tyr Ser Asn Ala Ala Tyr Met Ala Tyr Gly Tyr 50 55 60

Ala Ser Lys Thr Lys Leu Gly Ser Val Gly Gly Gln Thr Asp Ile Ser
 65 70 75 80
 Ile Asp Tyr Asn Ile Pro Cys Val Ser Ser Ser Gly Thr Phe Pro Cys
 85 90 95
 Pro Gln Glu Asp Ser Tyr Gly Asn Trp Gly Cys Lys Gly Met Gly Ala
 100 105 110
 Cys Ser Asn Ser Gln Gly Ile Ala Tyr Trp Ser Thr Asp Leu Phe Gly
 115 120 125
 Phe Tyr Thr Thr Pro Thr Asn Val Thr Leu Glu Met Thr Gly Tyr Phe
 130 135 140
 Leu Pro Pro Gln Thr Gly Ser Tyr Thr Phe Lys Phe Ala Thr Val Asp
 145 150 155 160
 Asp Ser Ala Ile Leu Ser Val Gly Gly Ala Thr Ala Phe Asn Cys Cys
 165 170 175
 Ala Gln Gln Gln Pro Pro Ile Thr Ser Thr Asn Phe Thr Ile Asp Gly
 180 185 190
 Ile Lys Pro Trp Gly Gly Ser Leu Pro Pro Asn Ile Glu Gly Thr Val
 195 200 205
 Tyr Met Tyr Ala Gly Tyr Tyr Tyr Pro Met Lys Val Val Tyr Ser Asn
 210 215 220
 Ala Val Ser Trp Gly Thr Leu Pro Ile Ser Val Thr Leu Pro Asp Gly
 225 230 235 240
 Thr Thr Val Ser Asp Asp Phe Glu Gly Tyr Val Tyr Ser Phe Asp Asp
 245 250 255
 Asp Leu Ser Gln Ser Asn Cys Thr Val Pro Asp Pro Ser Asn Tyr Ala
 260 265 270
 Val Ser Thr Thr Thr Thr Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr
 275 280 285
 Ser Thr Ser Thr Glu Met Thr Thr Val Thr Gly Thr Asn Gly Val Pro
 290 295 300
 Thr Asp Glu Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu
 305 310 315 320
 Ile Ser Thr Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser
 325 330 335
 Thr Glu Val Thr Thr Ile Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu
 340 345 350
 Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Ile Ser Thr
 355 360 365
 Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met
 370 375 380
 Thr Thr Val Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu Thr Val Ile
 385 390 395 400
 Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Val Thr Thr Thr Thr Glu
 405 410 415

Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met Ser Thr Val
 420 425 430
 Thr Gly Thr Asn Gly Leu Pro Thr Asp Glu Thr Val Ile Val Val Lys
 435 440 445
 Thr Pro Thr Thr Ala Ile Ser Ser Ser Leu Ser Ser Ser Ser Gly
 450 455 460
 Gln Ile Thr Ser Ser Ile Thr Ser Ser Arg Pro Ile Ile Thr Pro Phe
 465 470 475 480
 Tyr Pro Ser Asn Gly Thr Ser Val Ile Ser Ser Ser Val Ile Ser Ser
 485 490 495
 Ser Val Thr Ser Ser Leu Phe Thr Ser Ser Pro Val Ile Ser Ser Ser
 500 505 510
 Val Ile Ser Ser Ser Thr Thr Thr Ser Thr Ser Ile Phe Ser Glu Ser
 515 520 525
 Ser Lys Ser Ser Val Ile Pro Thr Ser Ser Ser Thr Ser Gly Ser Ser
 530 535 540
 Glu Ser Glu Thr Ser Ser Ala Gly Ser Val Ser Ser Ser Ser Phe Ile
 545 550 555 560
 Ser Ser Glu Ser Ser Lys Ser Pro Thr Tyr Ser Ser Ser Ser Leu Pro
 565 570 575
 Leu Val Thr Ser Ala Thr Thr Ser Gln Glu Thr Ala Ser Ser Leu Pro
 580 585 590
 Pro Ala Thr Thr Thr Lys Thr Ser Glu Gln Thr Thr Leu Val Thr Val
 595 600 605
 Thr Ser Cys Glu Ser His Val Cys Thr Glu Ser Ile Ser Pro Ala Ile
 610 615 620
 Val Ser Thr Ala Thr Val Thr Val Ser Gly Val Thr Thr Glu Tyr Thr
 625 630 635 640
 Thr Trp Cys Pro Ile Ser Thr Thr Glu Thr Thr Lys Gln Thr Lys Gly
 645 650 655
 Thr Thr Glu Gln Thr Thr Glu Thr Thr Lys Gln Thr Thr Val Val Thr
 660 665 670
 Ile Ser Ser Cys Glu Ser Asp Val Cys Ser Lys Thr Ala Ser Pro Ala
 675 680 685
 Ile Val Ser Thr Ser Thr Ala Thr Ile Asn Gly Val Thr Thr Glu Tyr
 690 695 700
 Thr Thr Trp Cys Pro Ile Ser Thr Thr Glu Ser Arg Gln Gln Thr Thr
 705 710 715 720
 Leu Val Thr Val Thr Ser Cys Glu Ser Gly Val Cys Ser Glu Thr Ala
 725 730 735
 Ser Pro Ala Ile Val Ser Thr Ala Thr Ala Thr Val Asn Asp Val Val
 740 745 750
 Thr Val Tyr Pro Thr Trp Arg Pro Gln Thr Ala Asn Glu Glu Ser Val
 755 760 765

Ser Ser Lys Met Asn Ser Ala Thr Gly Glu Thr Thr Thr Asn Thr Leu
 770 775 780
 Ala Ala Glu Thr Thr Thr Asn Thr Val Ala Ala Glu Thr Ile Thr Asn
 785 790 795 800
 Thr Gly Ala Ala Glu Thr Lys Thr Val Val Thr Ser Ser Leu Ser Arg
 805 810 815
 Ser Asn His Ala Glu Thr Gln Thr Ala Ser Ala Thr Asp Val Ile Gly
 820 825 830
 His Ser Ser Ser Val Val Ser Val Ser Glu Thr Gly Asn Thr Lys Ser
 835 840 845
 Leu Thr Ser Ser Gly Leu Ser Thr Met Ser Gln Gln Pro Arg Ser Thr
 850 855 860
 Pro Ala Ser Ser Met Val Gly Tyr Ser Thr Ala Ser Leu Glu Ile Ser
 865 870 875 880
 Thr Tyr Ala Gly Ser Ala Thr Ala Tyr Trp Pro Val Val Val
 885 890

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ChoB template coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGCCCCAGCC GCACCCTCG

19

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: ChoB template non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CGAGGGTGCC GCTGGGGGC

19

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: cho01pcr primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGATCTGAAT TCGCGGCCGC CCCAGCCGC ACCCTCG

37

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: cho02pcr primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGATCTAAGC TTTCAGCTAG CCTGGATGTC GGACGAGATG AT

42

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ChoB template coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATCATCTCGT CCGACATCCA G

21

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ChoB template non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGGATGTCG GACGAGATGA T

21

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: mutagenesis primer ChoB

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGCGGCGACG GCACCGCCGT ATGCACTGGC GATGACGAGG GC

42

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: ChoB template coding strand

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GCCCTCGTCA TCGGCAGTGG ATACGGCGGT GCCGTCGCCG CG

42

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: primer prt1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AAGATCTATC GATCTTGTTA GCCGGTACA

29

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: proteinase template non-coding strand

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACTGTACCG GCTAACAAGA TCGATAGCCC TT

32

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: proteinase template coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTCGGCGAAA TCCAAGCAAA GCGGGCT

27

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: prt2 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CCCAAGCTTC CCCCCGGCCG TTGCTTGGAT TTCGCCGAC

39

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: EGf1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGGGCGGCCG CGCTGGAGGA AAAGAAAGTT TGC

33

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: EGF receptor template non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCAAACTTTC TTTTCTCCA GAGCCCGACT CGC

33

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: EGF receptor template coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AATGGGCCTA AGATCCCGTC CATCGCCACT

30

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: EGF2 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCCCAAGCTT AAGGCTAGCG GACGGGATCT TAGGCCCAT

40

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vhc - AGal linker with MycT and Hinge

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAATTCAGG TCACCGTCTC CTCAGAACA AACTCATCT CAGAAGAGGA TCTGAATGAA 60

CCAAAGATTC CACAACCTCA ACCAAAGCCA CAACCTCAAC CACAACCACA ACCAAAACCT 120

CAACCAAAGC CAGAACCAGA ATCTACTTCC CCAAAGTCTC CAGCTAGCCT TAAGCTT 177

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vhc - AGal linker with MycT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GAATTCCAGG TCACCGTCTC CTCAGAACAA AAATCATCT CAGAAGAGGA TCTGAATGCT 60
AGC 63

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vhc - AGal linker with Hinge

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GAATTCCAGG TCACCGTCTC CTCAGAACCA AAGATTCCAC AACCTCAACC AAAGCCACAA 60
CCTCAACCAC AACCACAACC AAAACCTCAA CCAAAGCCAG AACCAGAATC TACTTCCCCA 120
AAGTCTCCAG CTAGCCTTAA GCTT 144

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: fragment in pUR4421 coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTTAGCGG CCGCCCAGGT GAAACTGCTC GAGTAAGTGA CTAAGGTCAC CGTCTCCTCA 60
GAACAAAAC TCATCTCAGA AGAGGATCTG AATTAATGAG AATTCATCAA ACGGTGATA 119

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: fragment in pUR4421 non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AGCTTATCAC CGTTTGATGA ATTCTCATTA ATTCAGATCC TCTTCTGAGA TGAGTTTTTG 60
TTCTGAGGAG ACGGTGACCT TAGTCACTTA CTCGAGCAGT TTCACCTGGG CGGCCGCTA 119

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: Myc tail

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BstEII-HindIII linker coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTCACCGTCT CCTCATAATG A

21

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BstEII HindIII linker non-coding strand

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGCTTCATTA TGAGGAGACG

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: primer cho03pcr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGGATCCAAG CTTGAGCCTG GATGTCGGAC GAGATGAT

38

C L A I M S

1. A method for immobilizing a binding protein capable of binding to a specific compound, comprising the use of recombinant DNA techniques for producing said binding protein or a functional part thereof still having said specific binding capability, said protein or said part thereof being linked to the outside of a host cell, whereby said binding protein or said part thereof is localized in the cell wall or at the exterior of the cell wall by allowing the host cell to produce and secrete a chimeric protein in which said binding protein or said functional part thereof is bound with its C-terminus to the N-terminus of an anchoring part of an anchoring protein capable of anchoring in the cell wall of the host cell, which anchoring part is derivable from the C-terminal part of said anchoring protein.

2. The method of claim 1, in which the host is selected from the group consisting of Gram-positive bacteria and fungi.

3. The method of claim 2, in which the host is a Gram-positive bacterium selected from the group consisting of lactic acid bacteria, and bacteria belonging to the genera *Bacillus* and *Streptomyces*.

4. The method of claim 2, in which the host is a fungus selected from the group consisting of yeasts belonging to the genera *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* and *Saccharomyces*, and moulds belonging to the genera *Aspergillus*, *Penicillium* and *Rhizopus*.

5. A recombinant polynucleotide comprising

- (i) a structural gene encoding a binding protein or a functional part thereof still having the specific binding capability, and
- (ii) at least part of a gene encoding an anchoring protein capable of anchoring in the cell wall of a Gram-positive bacterium or a fungus, said part of a gene encoding at least the anchoring part of said anchoring protein, which

anchoring part is derivable from the C-terminal part of said anchoring protein.

6. The polynucleotide of claim 5, wherein the anchoring protein is selected from the group consisting of α -agglutinin, α -agglutinin, FLO1, the Major Cell Wall Protein of a fungus, and proteinase of lactic acid bacteria.

7. The polynucleotide of claim 5, further comprising a nucleotide sequence encoding a signal peptide ensuring secretion of the expression product of the polynucleotide.

8. The polynucleotide of claim 7, wherein the signal peptide is derived from a protein selected from the group consisting of the α -mating factor of yeast, α -agglutinin of yeast, invertase of *Saccharomyces*, inulinase of *Kluyveromyces*, α -amylase of *Bacillus*, and proteinase of lactic acid bacteria.

9. The polynucleotide of any of claims 5-8, operably linked to a promoter, which can be an inducible promoter.

10. A recombinant vector comprising a polynucleotide as claimed in any of claims 5-9.

11. A chimeric protein encoded by a polynucleotide as claimed in any of claims 5-9.

12. A host cell having a cell wall at the outside of its cell and containing at least one polynucleotide as claimed in any of claims 5-9.

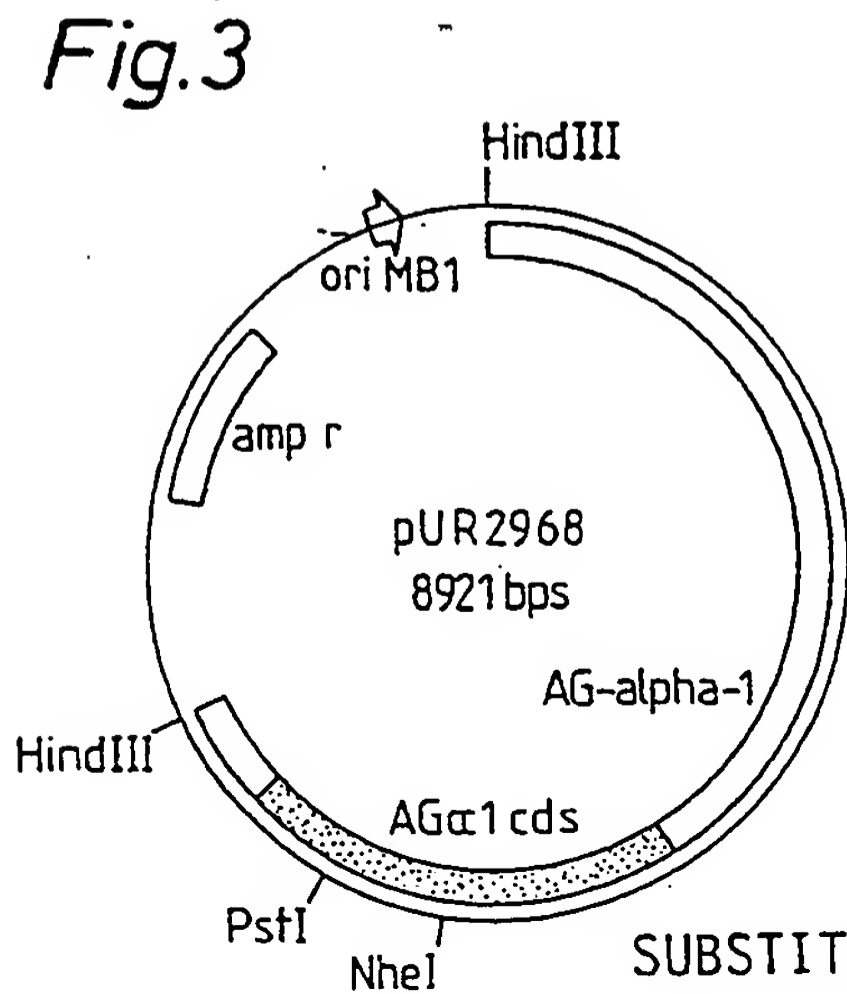
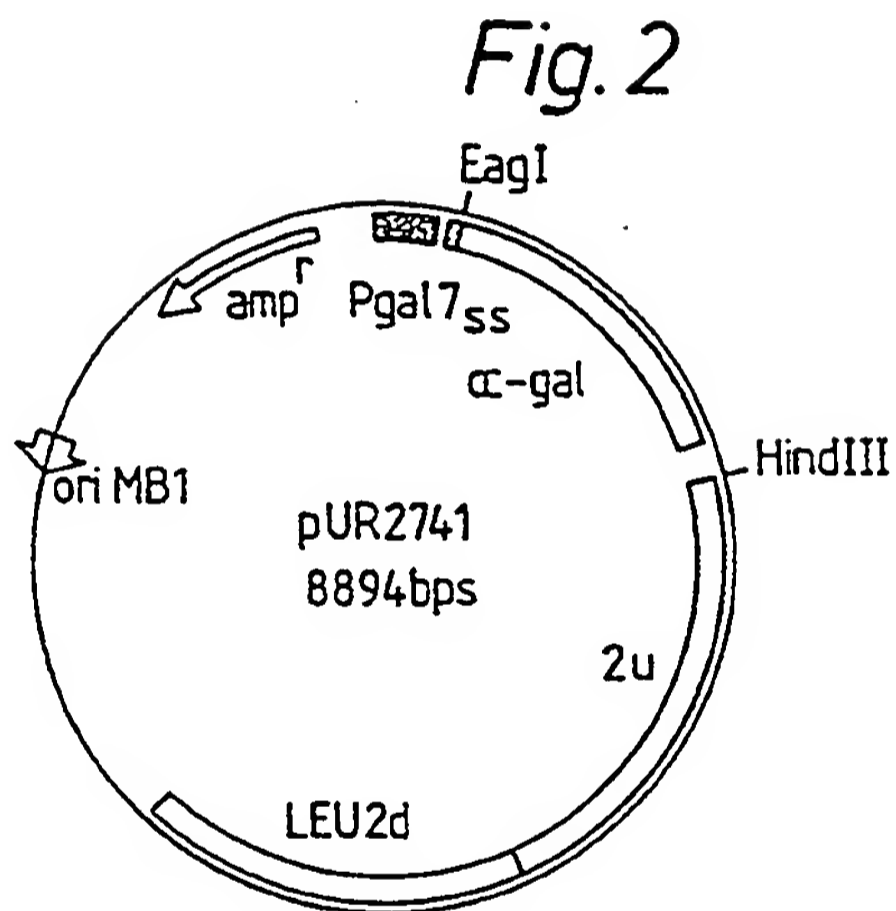
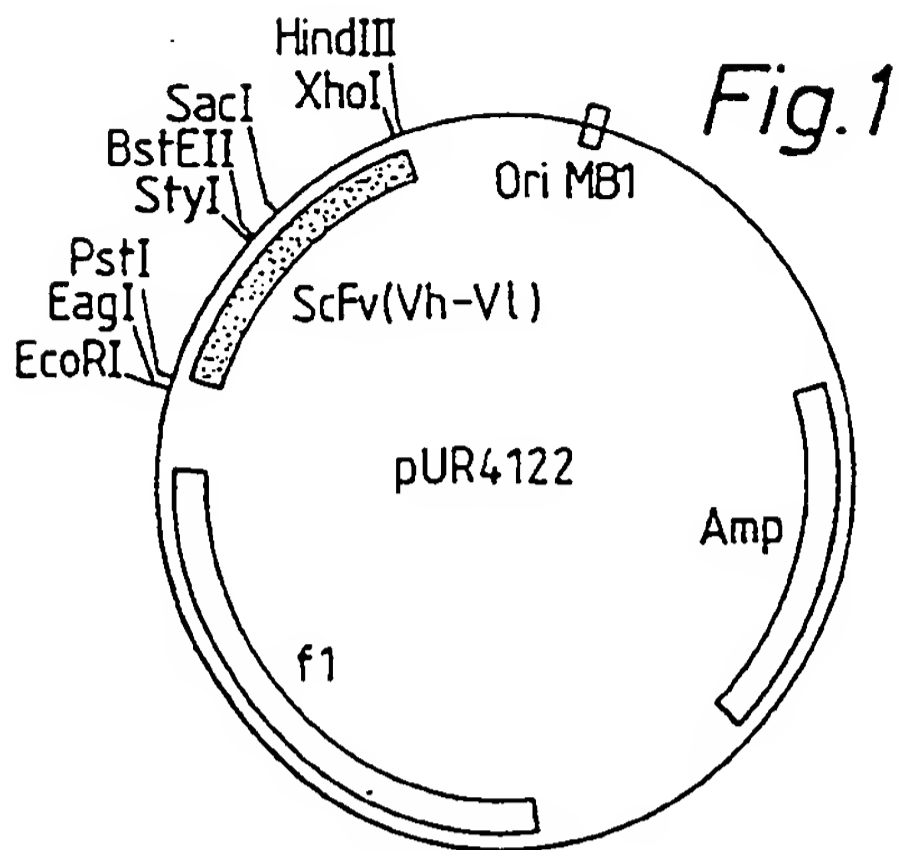
13. The host cell of claim 12, having at least one polynucleotide as claimed in any of claims 5-9 integrated in its chromosome.

14. A host cell having a chimeric protein as claimed in claim 11 immobilized in its cell wall and having the binding protein part of the chimeric protein localized in the cell wall or at the exterior of the cell wall.

15. The host cell of any of claims 12-14, which is a fungus selected from the group consisting of yeasts and moulds.

16. A process for carrying out an isolation process by using an immobilized binding protein or functional part thereof still capable of binding to a specific compound, wherein a medium containing said specific compound is contacted with a host cell as claimed in any of claims 12-15 under conditions whereby a complex between said specific compound and said immobilized binding protein is formed, separating said complex from the medium originally containing said specific compound and, optionally, releasing said specific compound from said binding protein or functional part thereof.

* * * * *



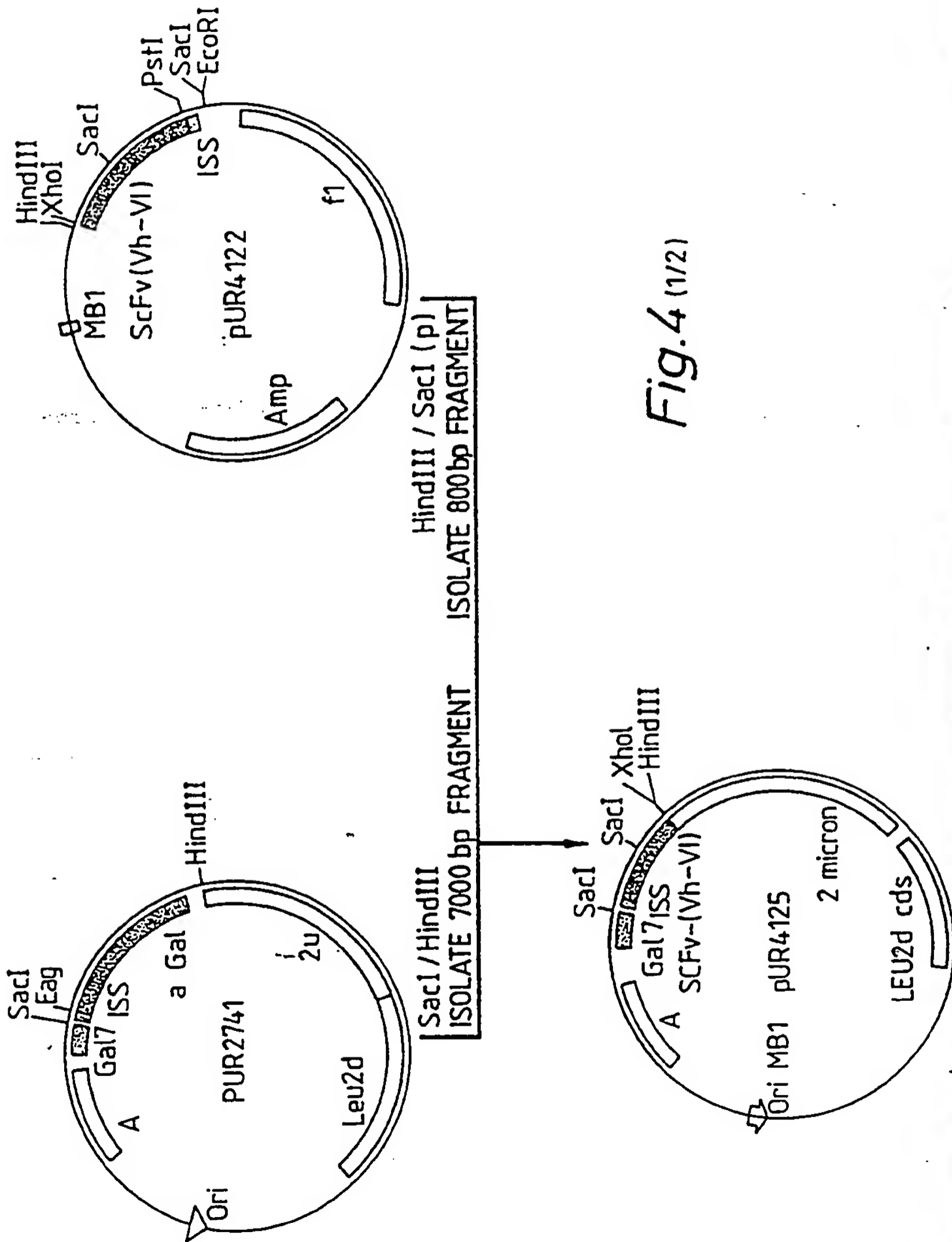


Fig. 4 (1/2)

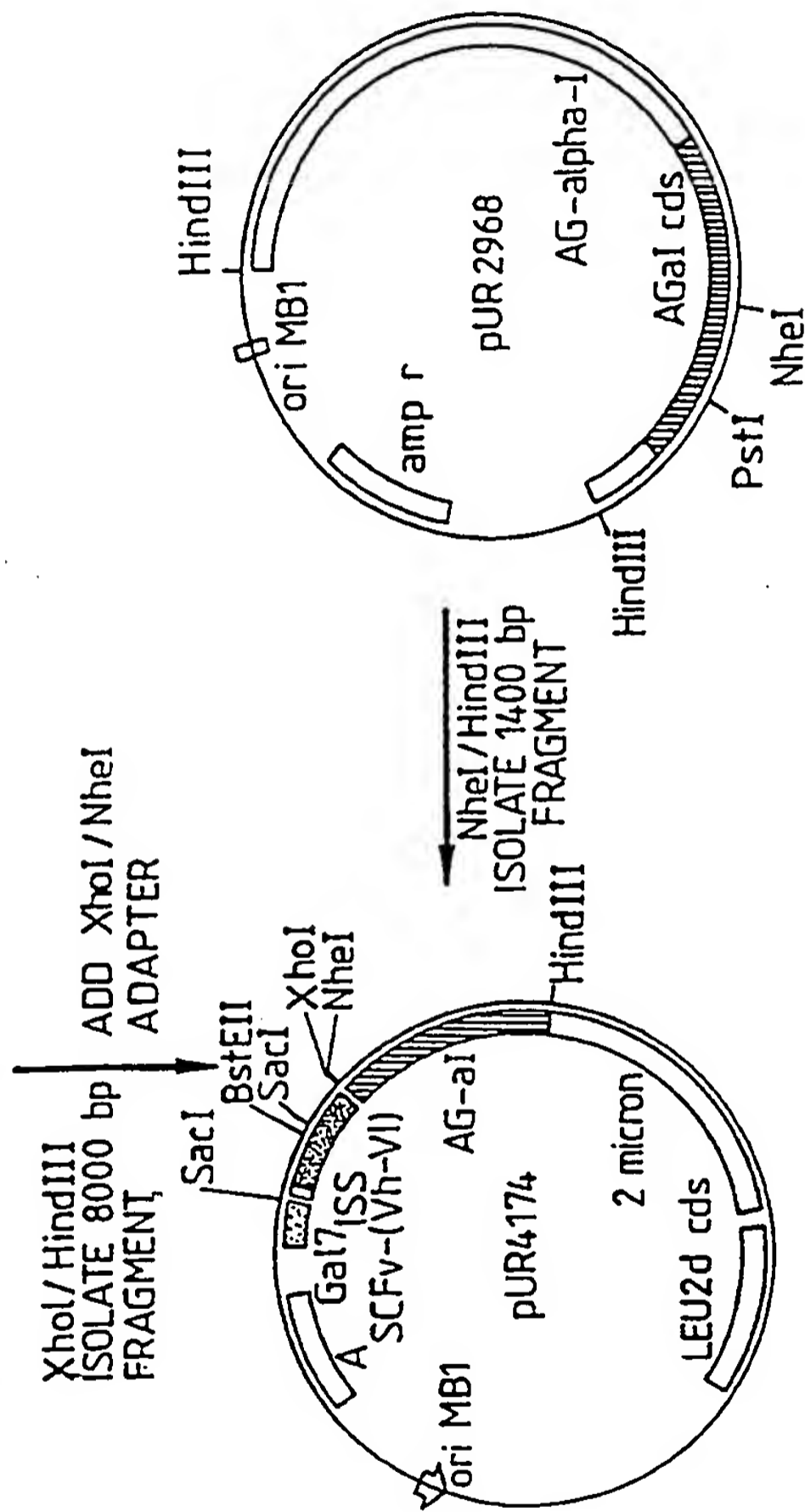


Fig. 4 (1/2) (Cont.)

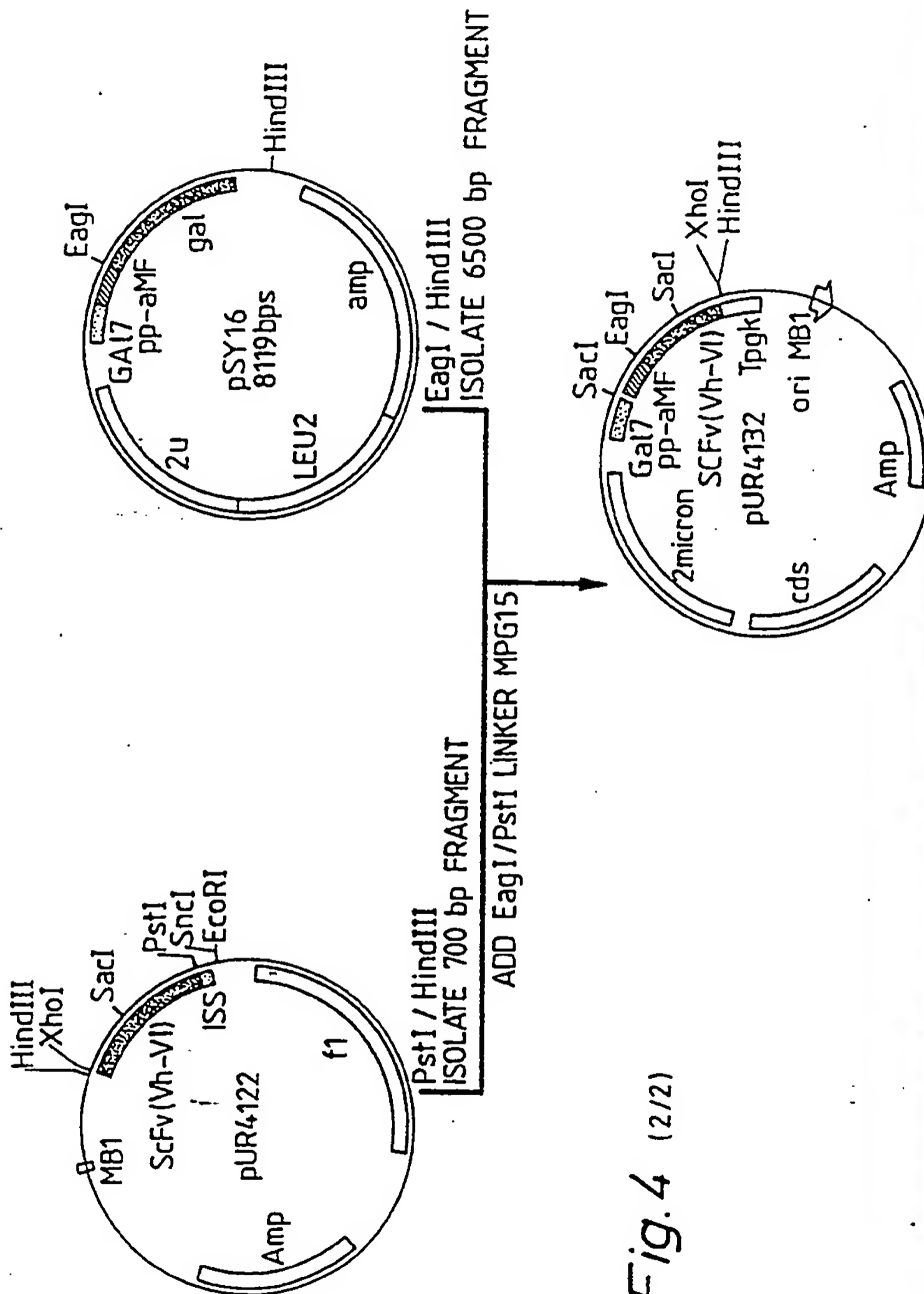


Fig. 4 (2/2)

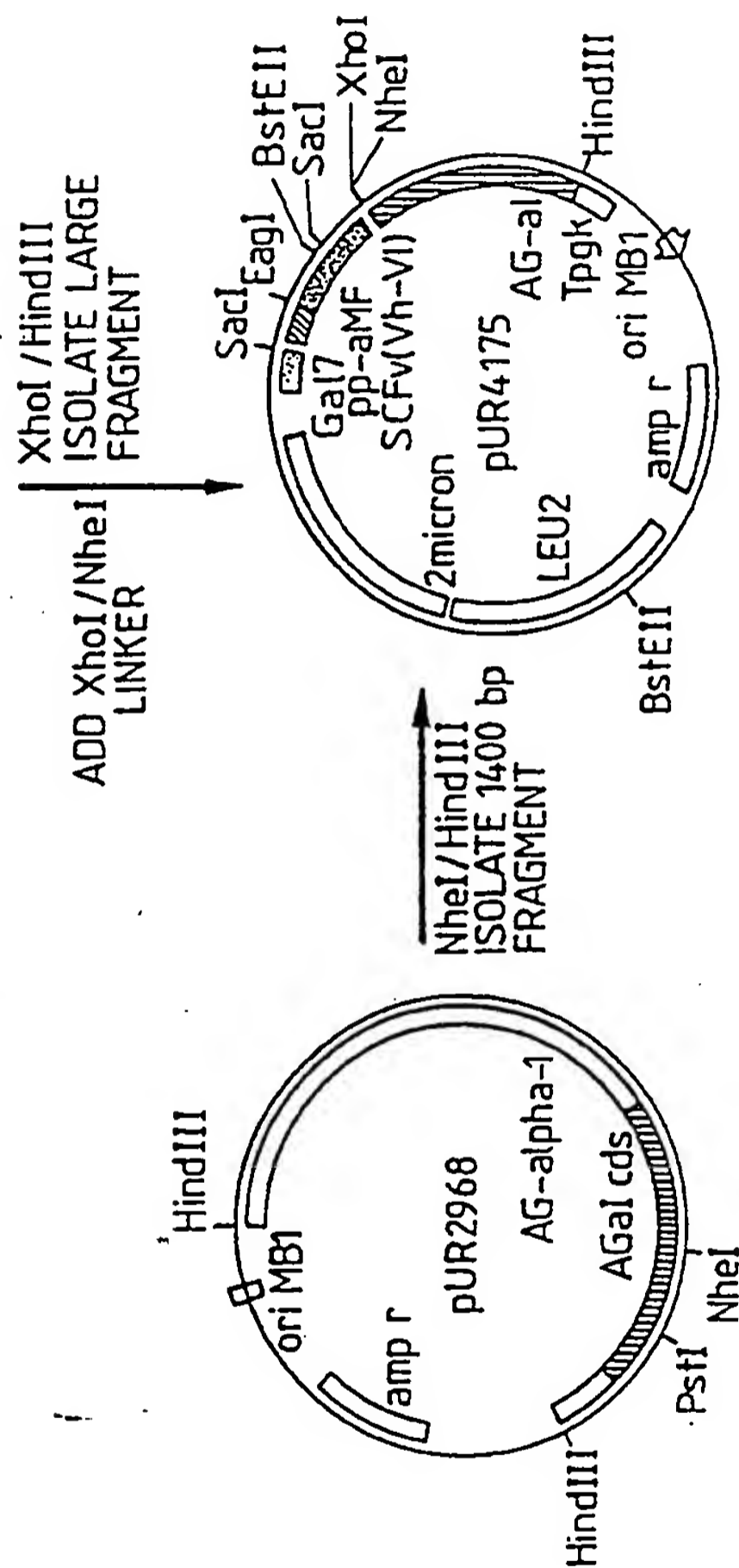
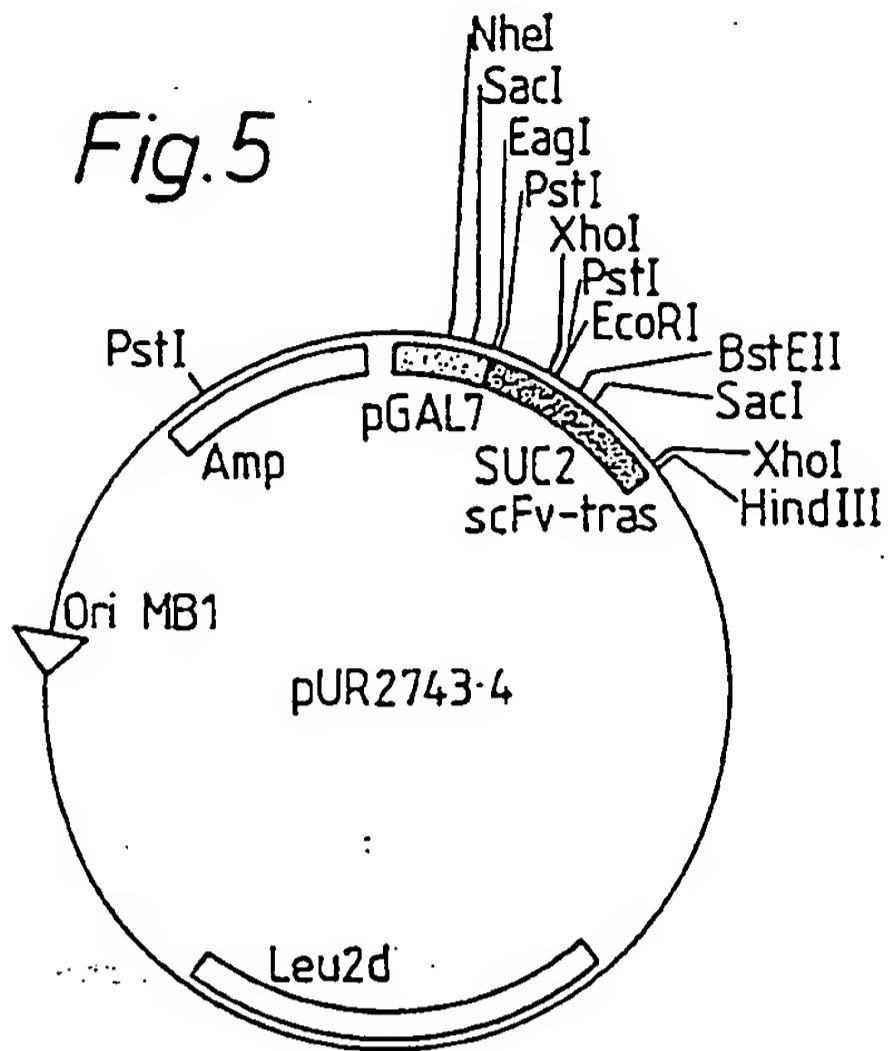
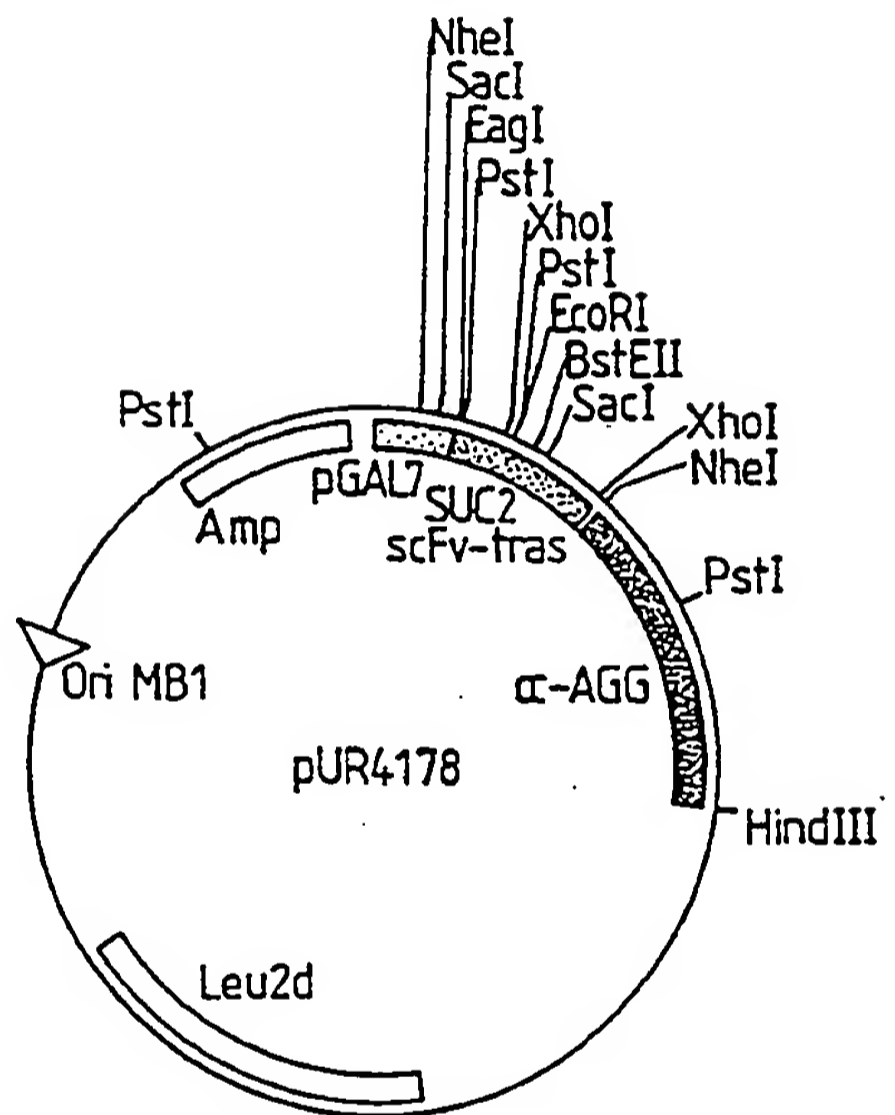
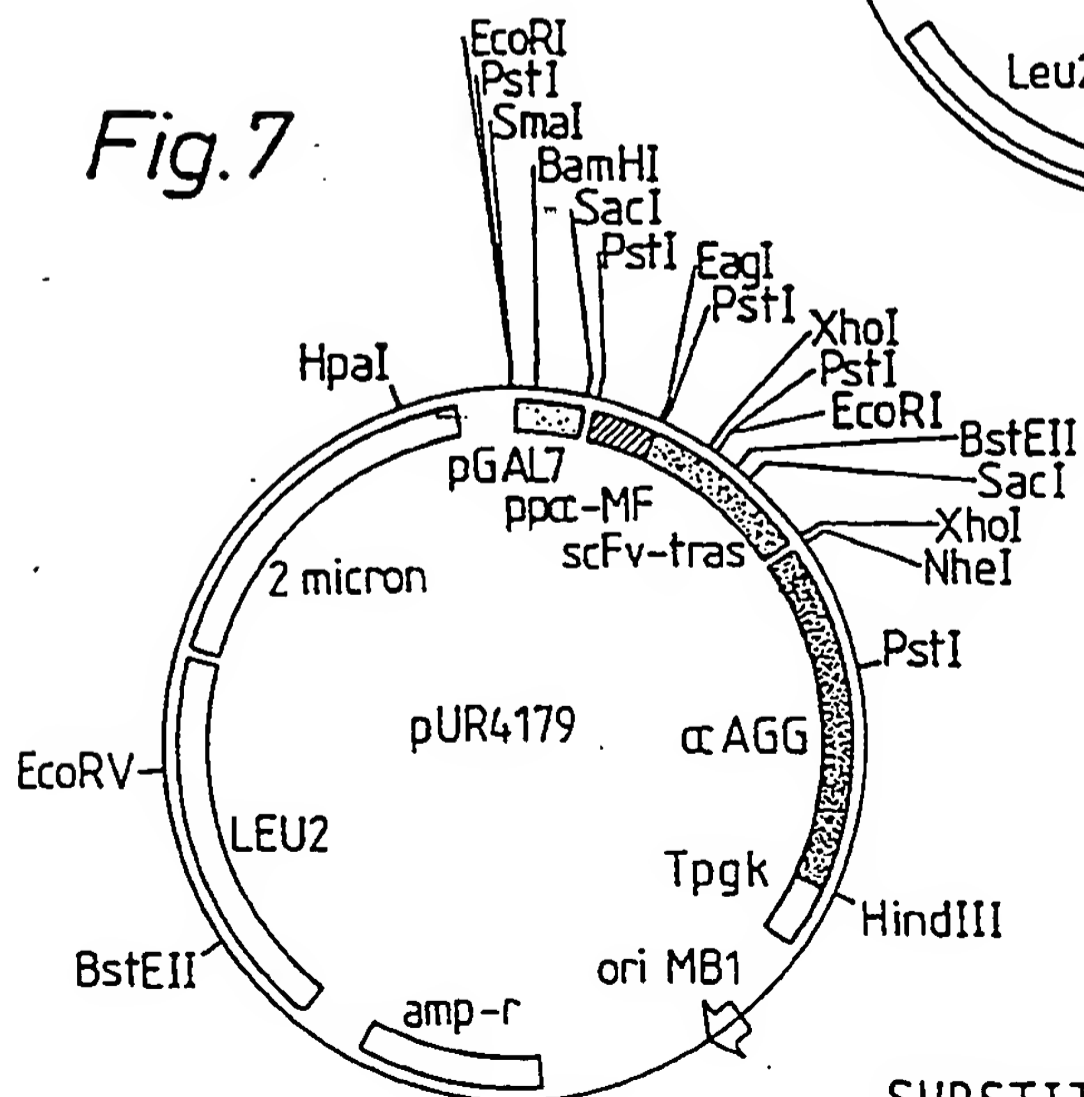


Fig. 4 (2/2) (Cont.)

Fig. 5*Fig. 6**Fig. 7*

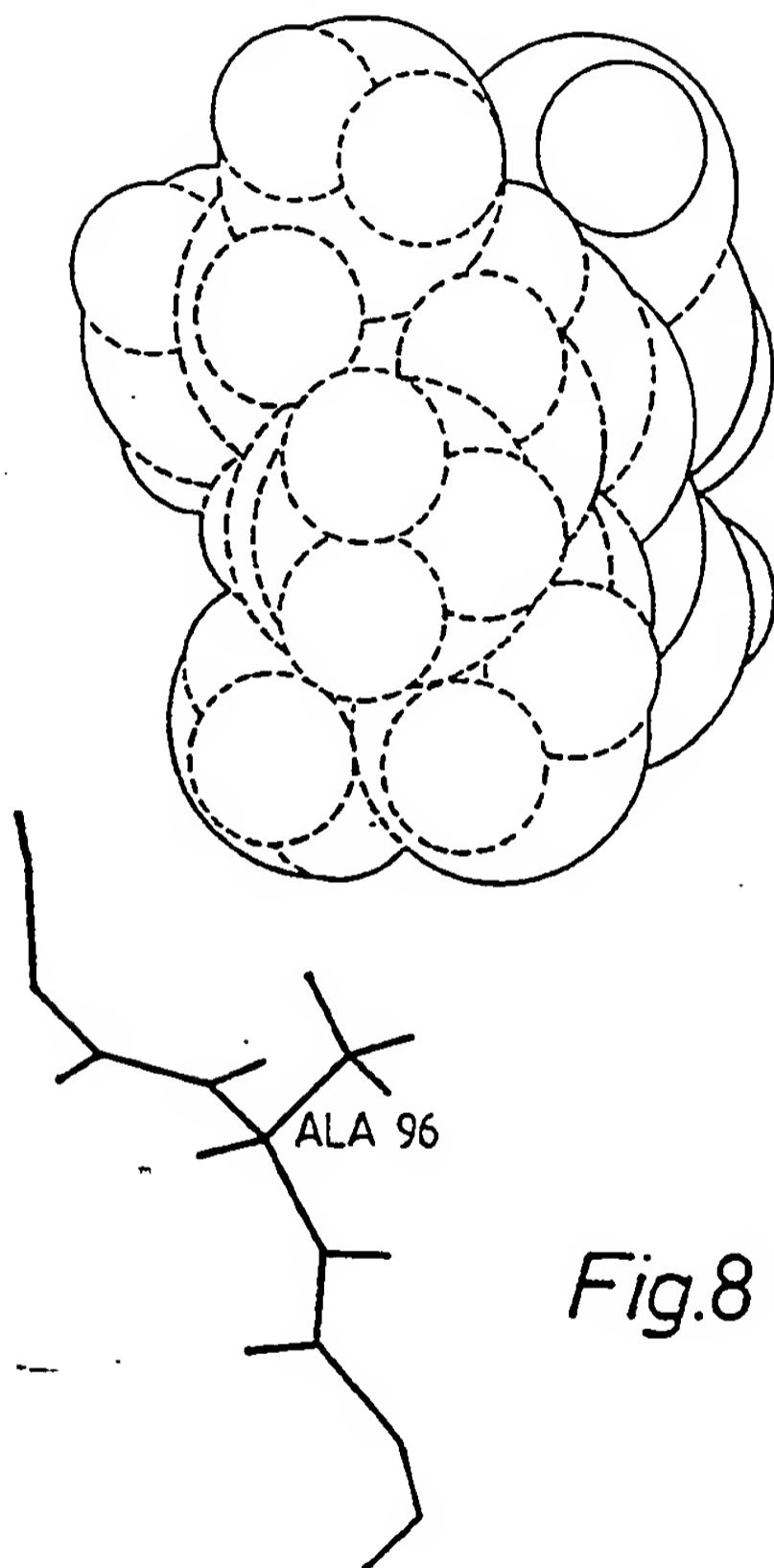
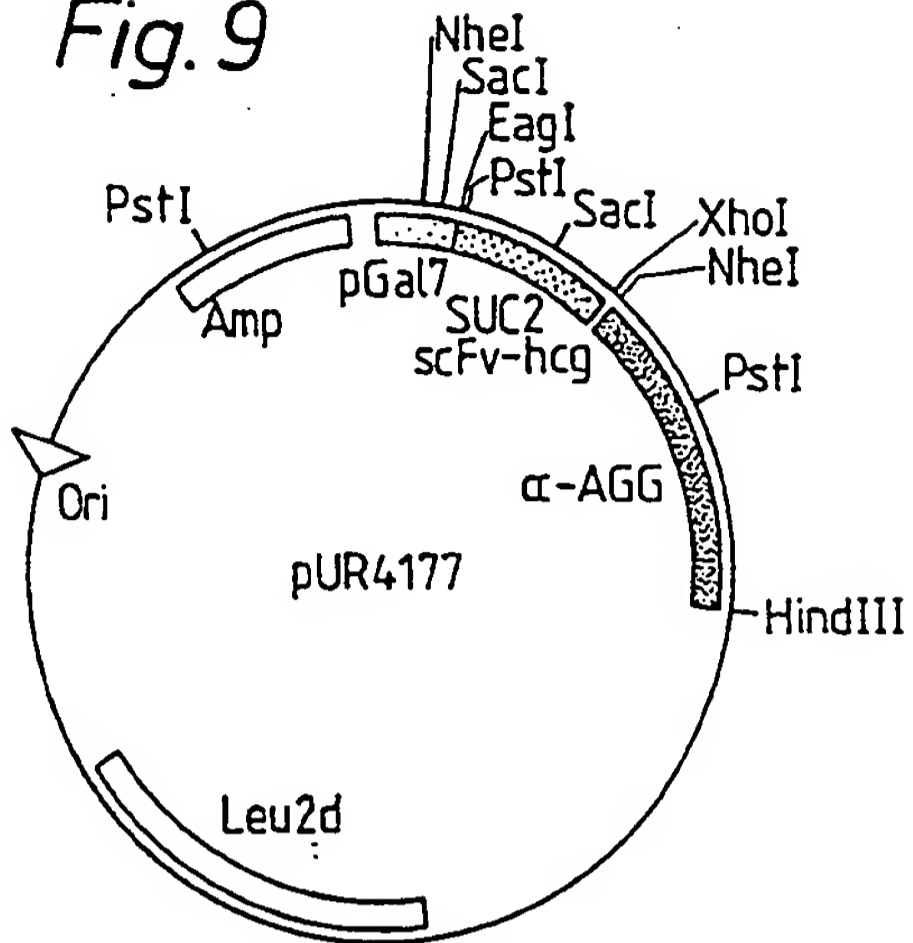
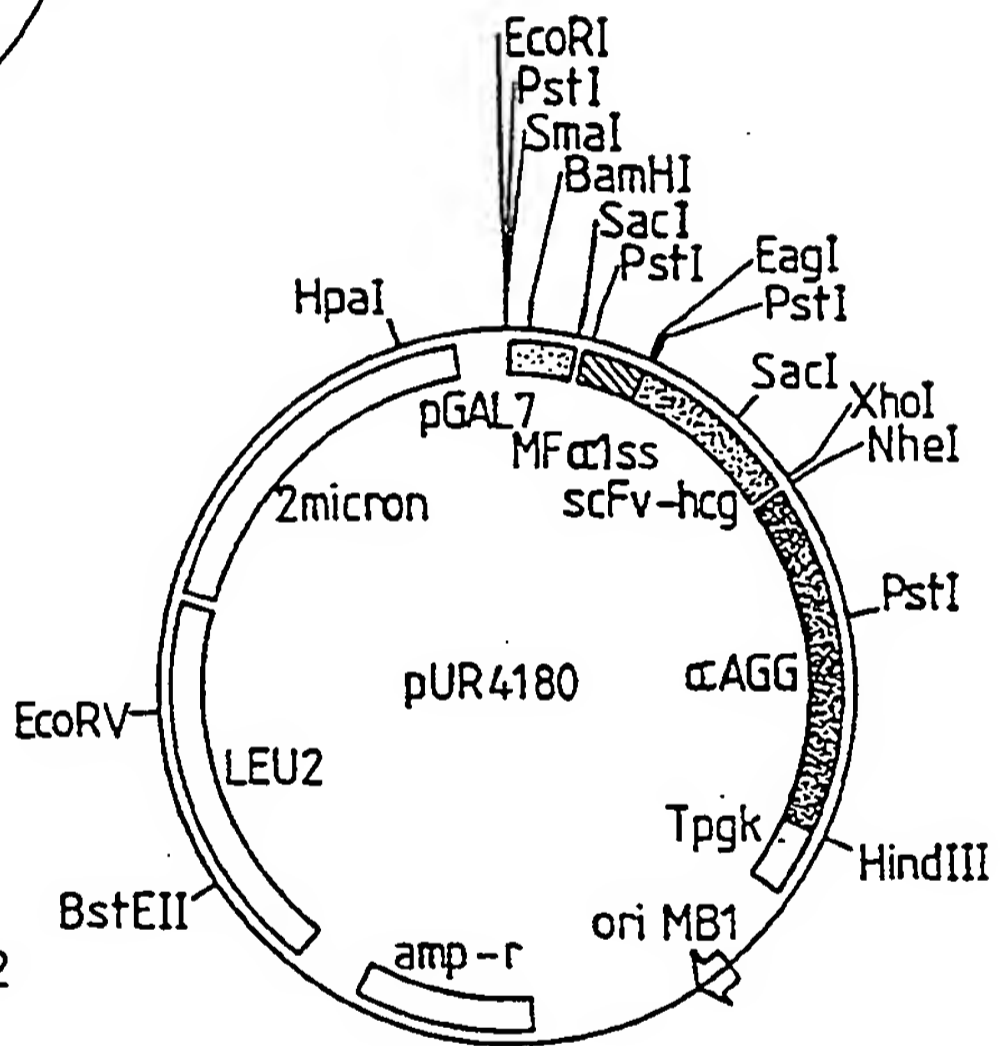
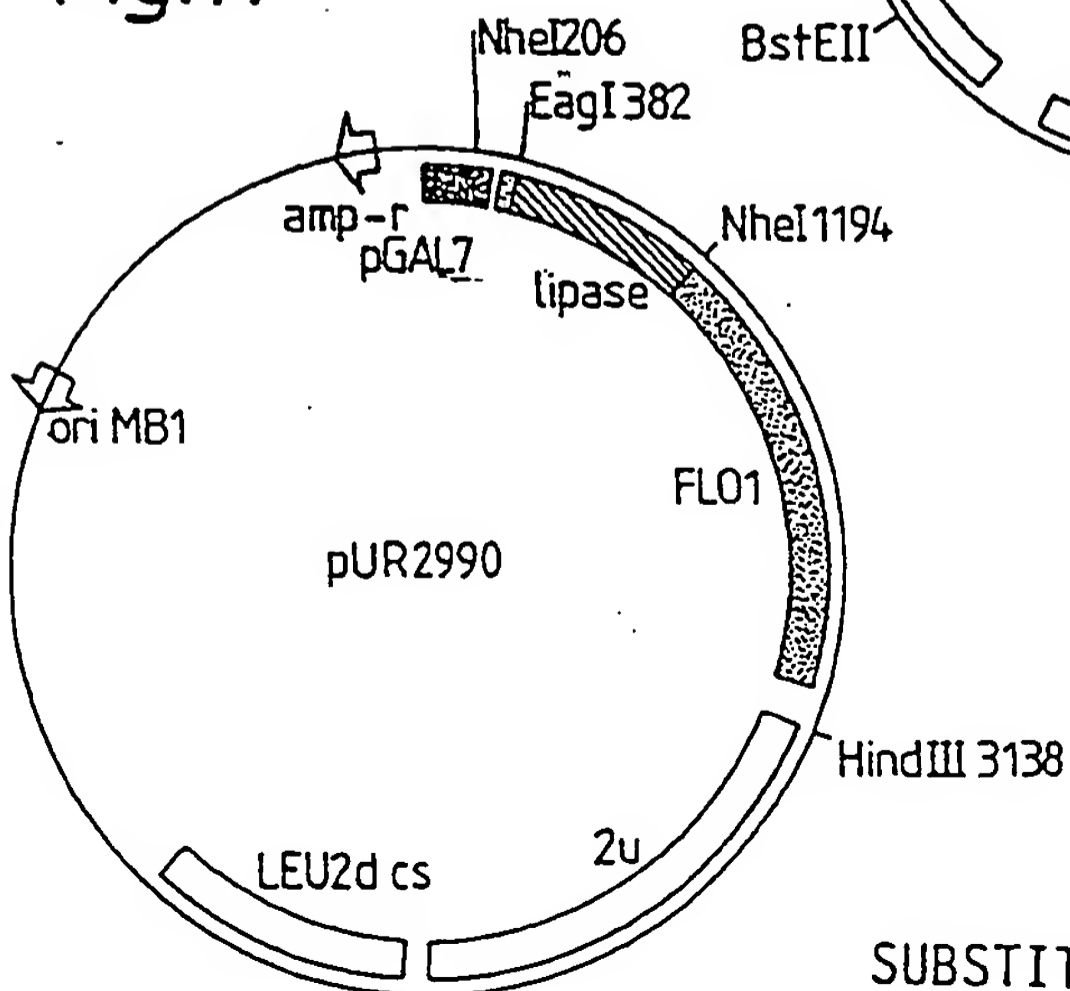
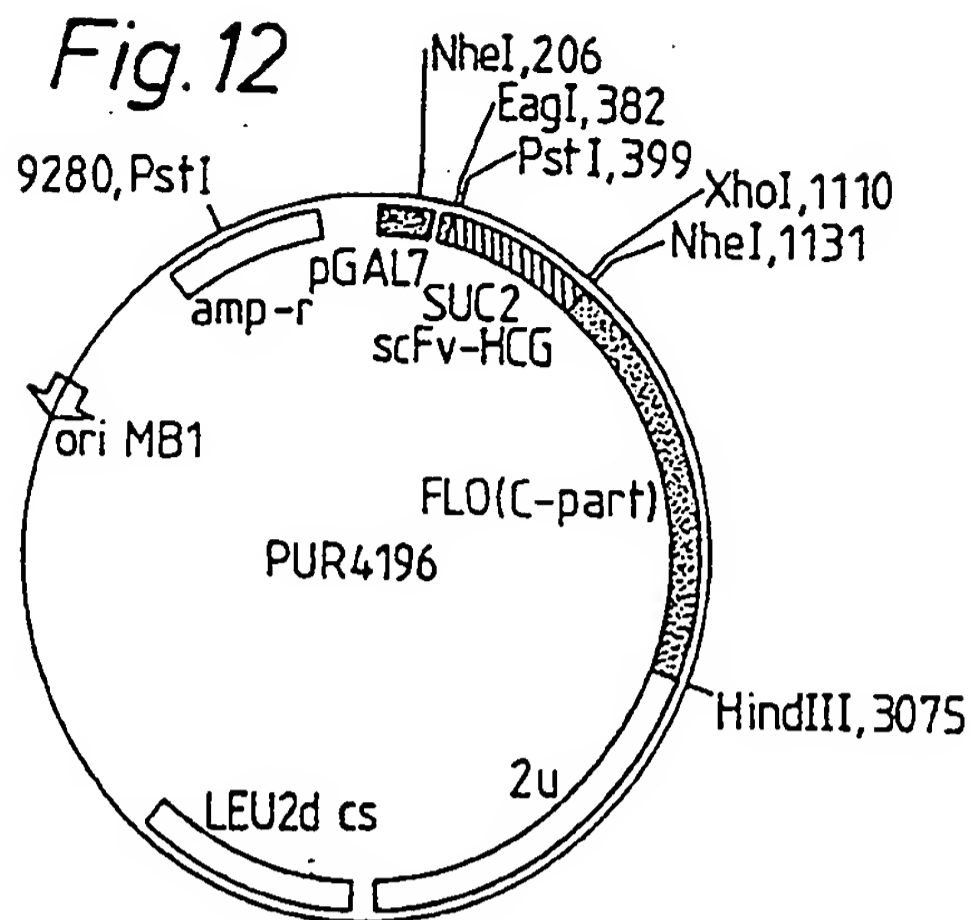
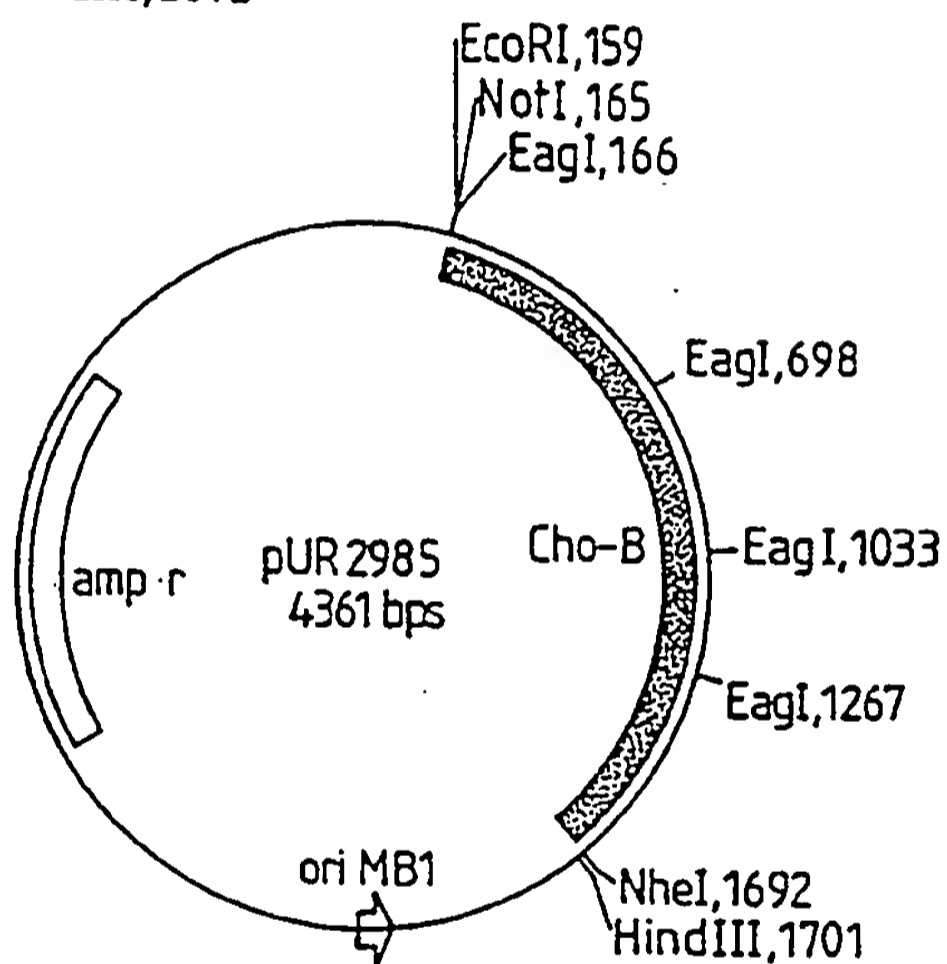
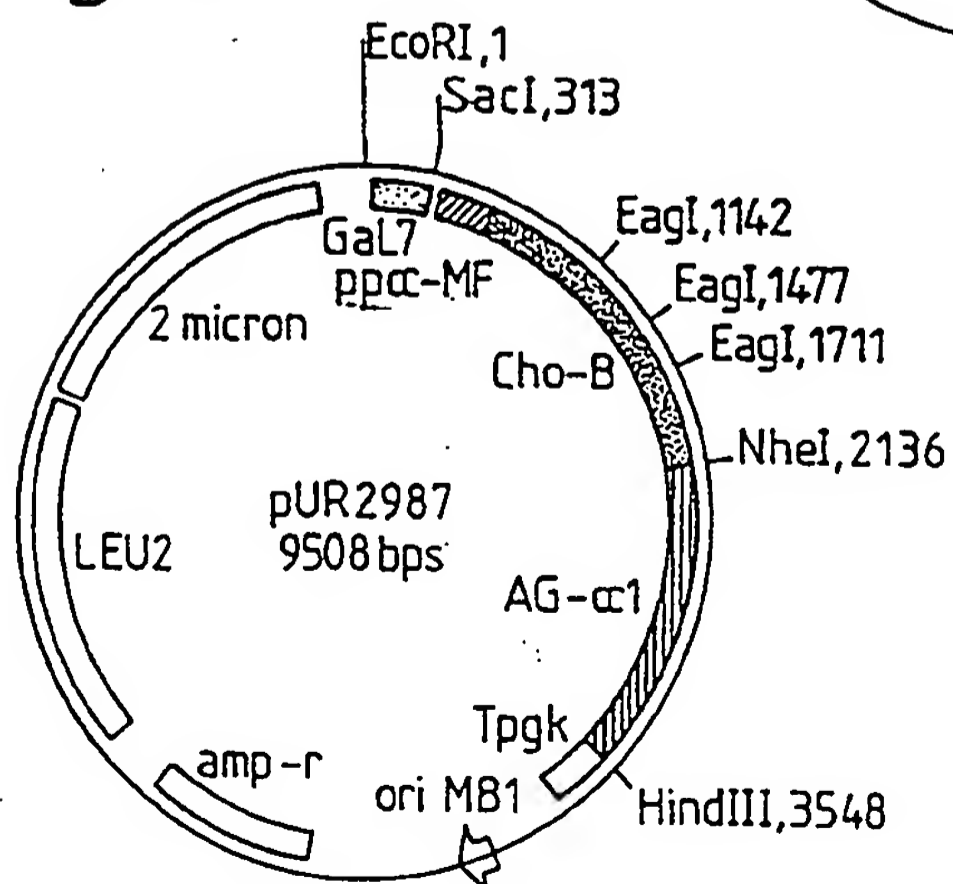
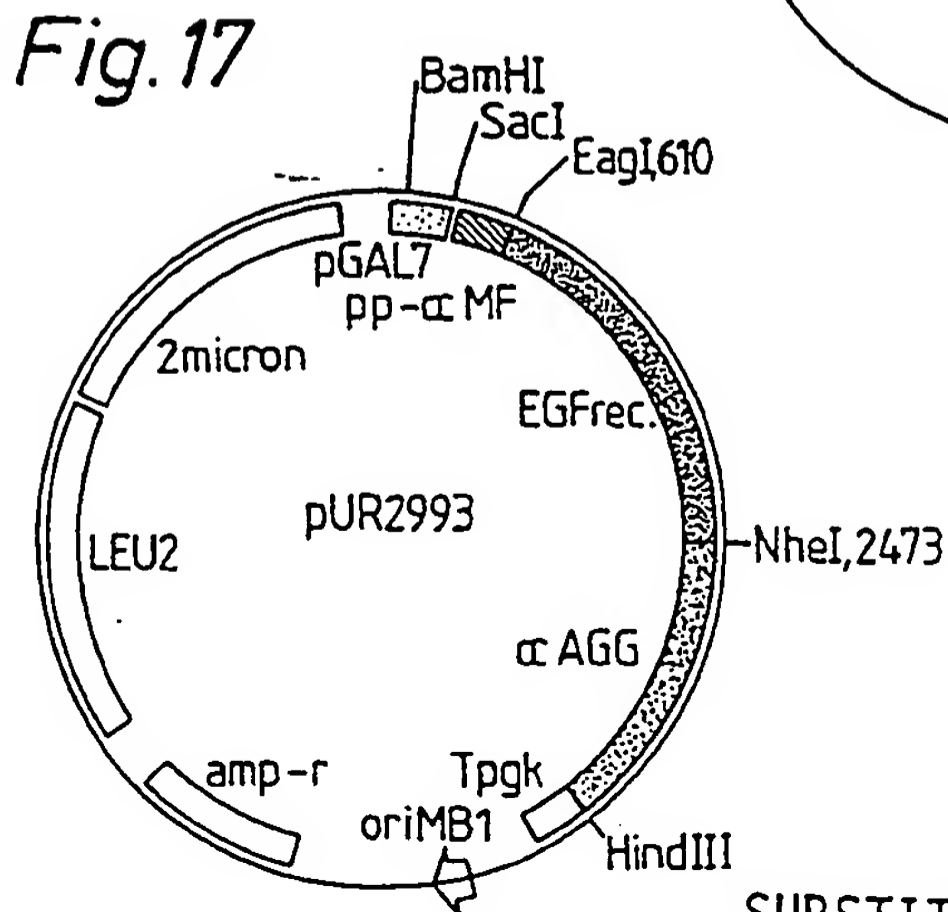
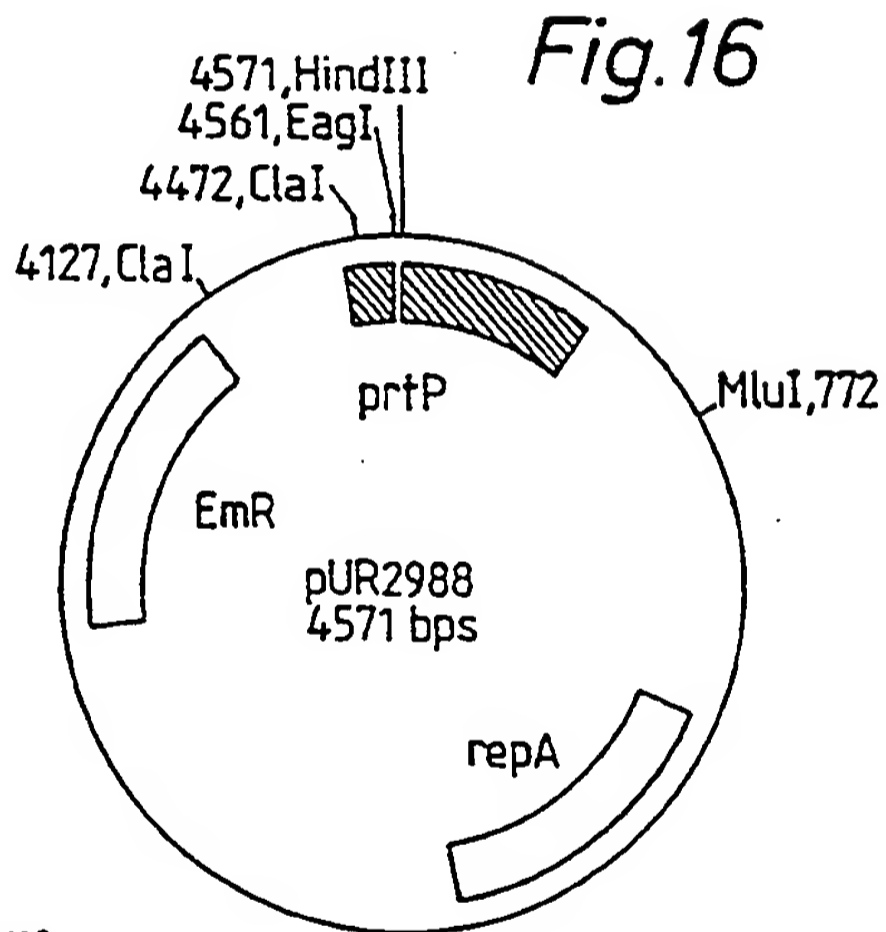
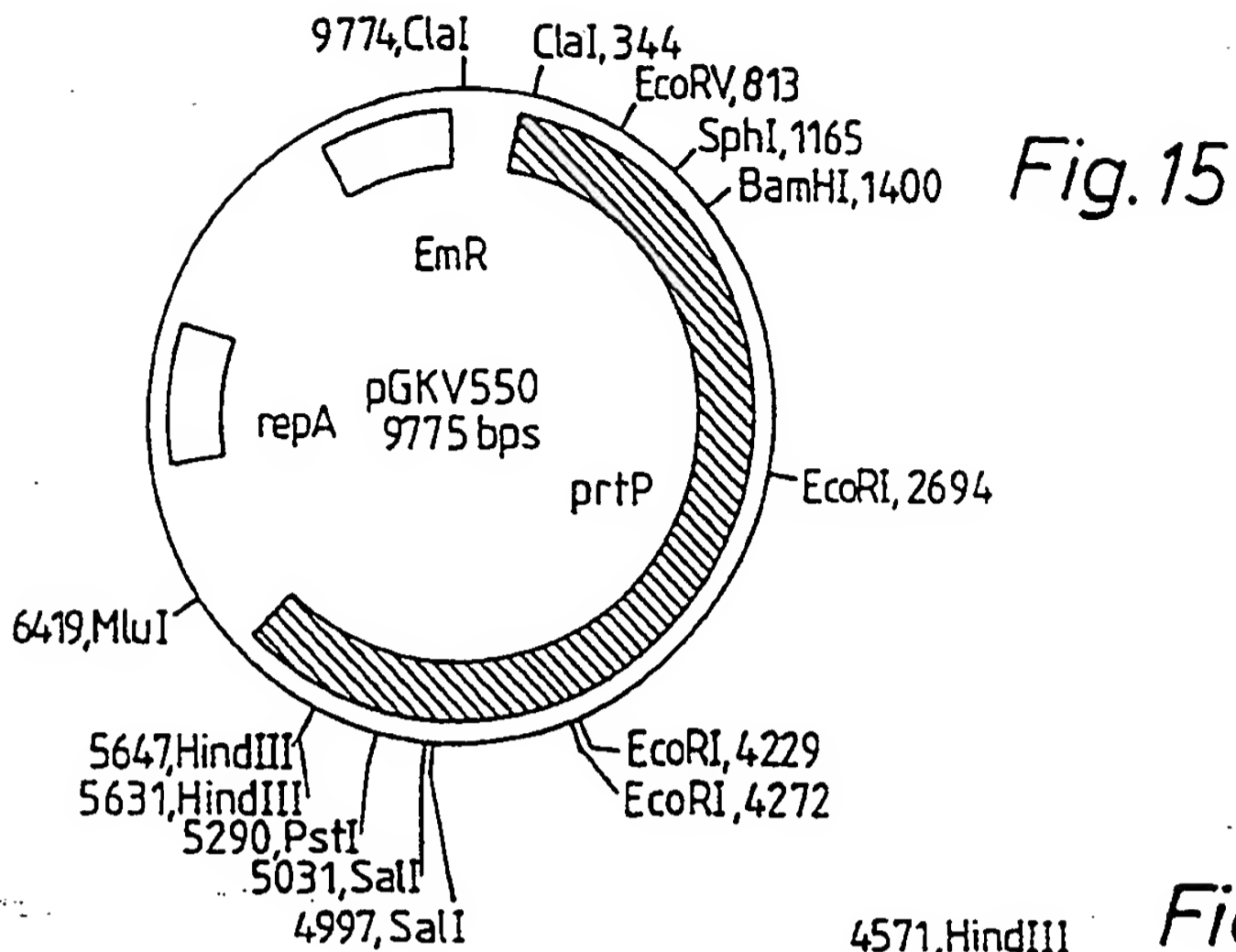
*Fig.8*

Fig. 9*Fig. 10**Fig. 11*

**Fig. 13****Fig. 14**



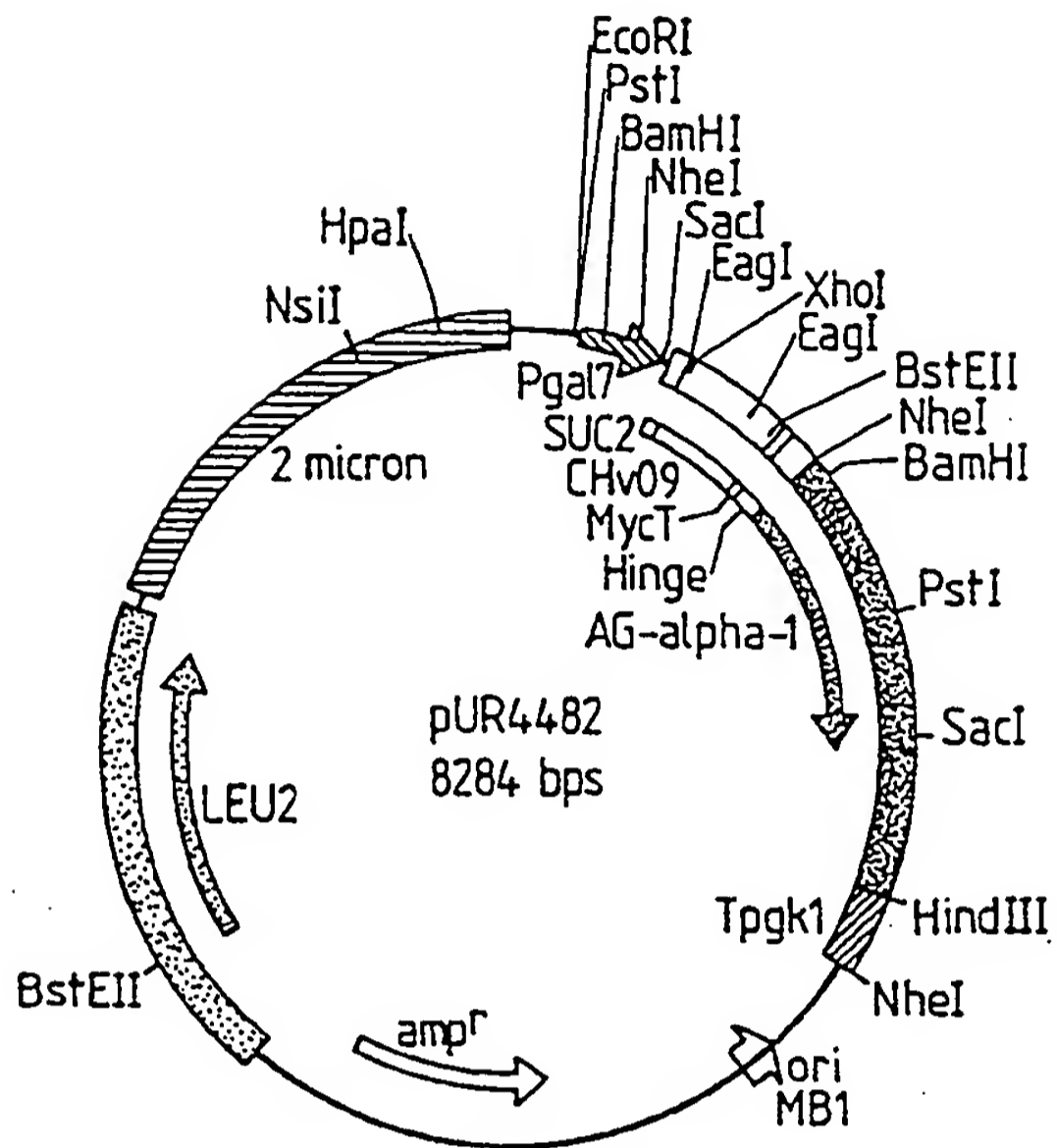


Fig. 18

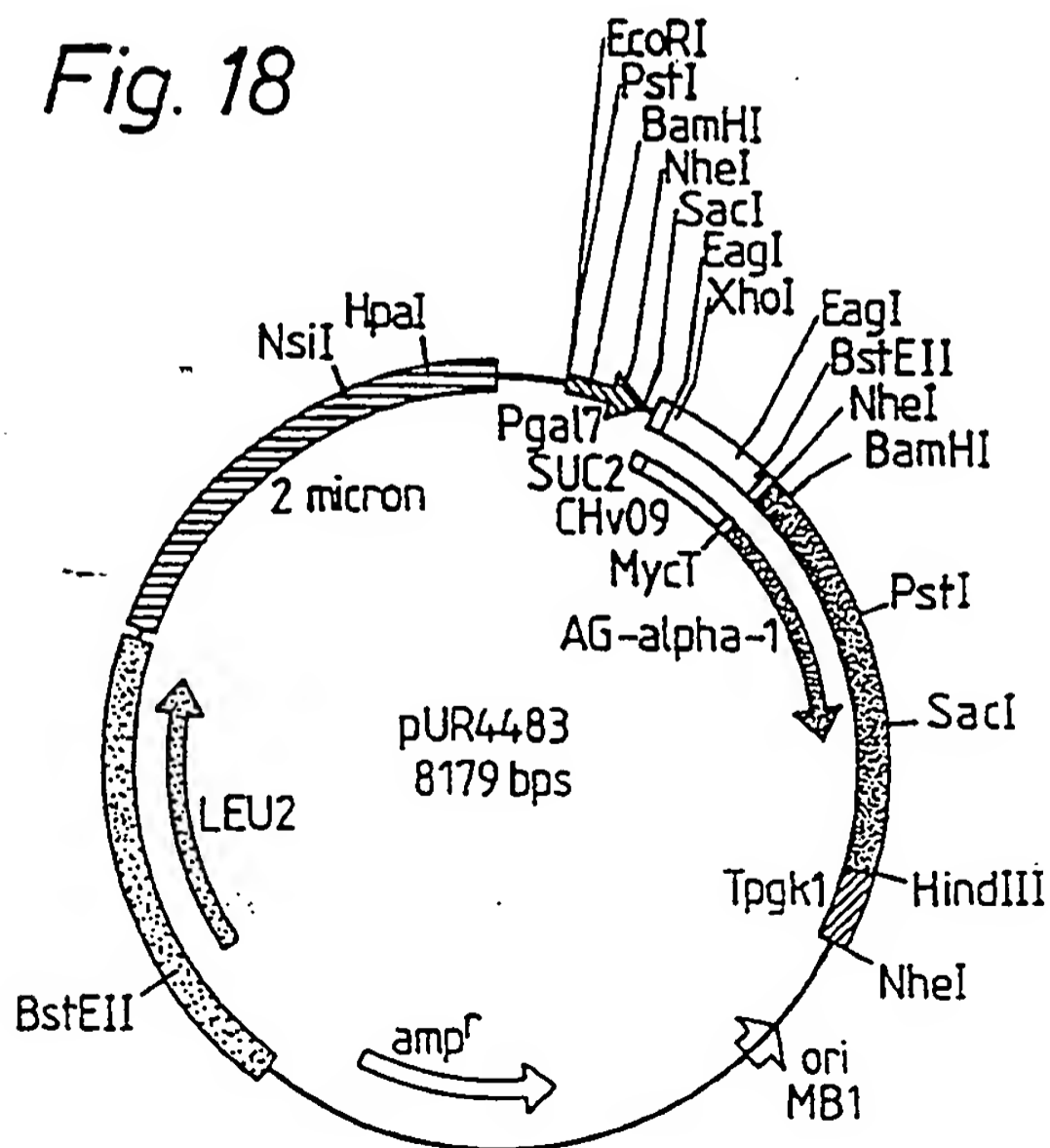
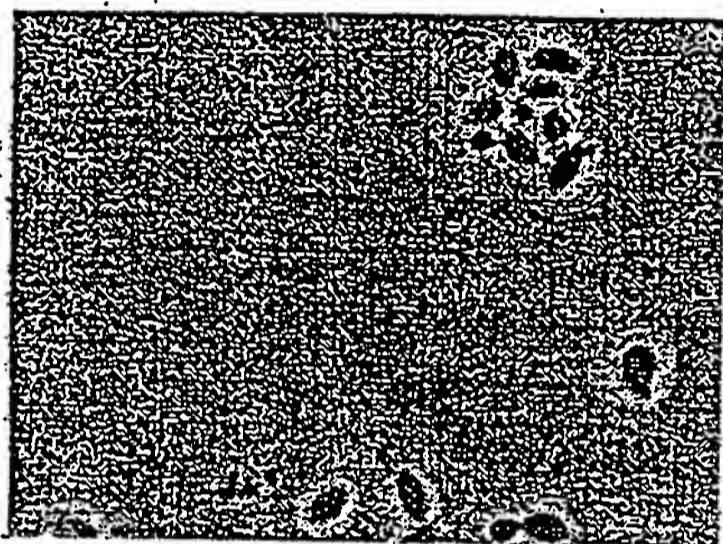
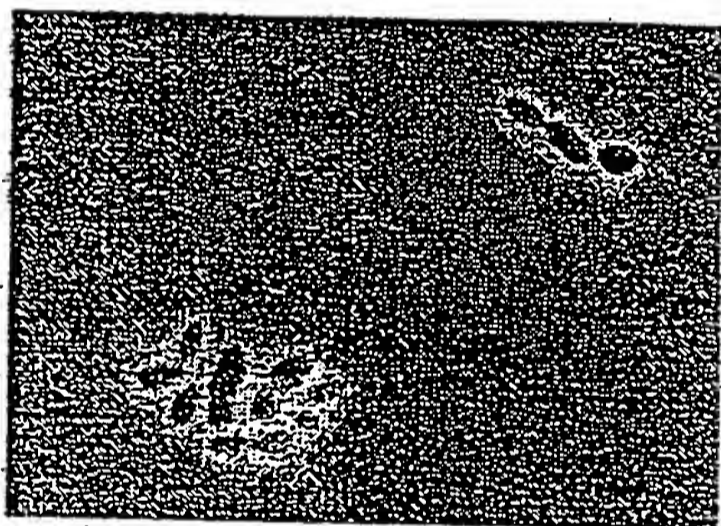


Figure 19



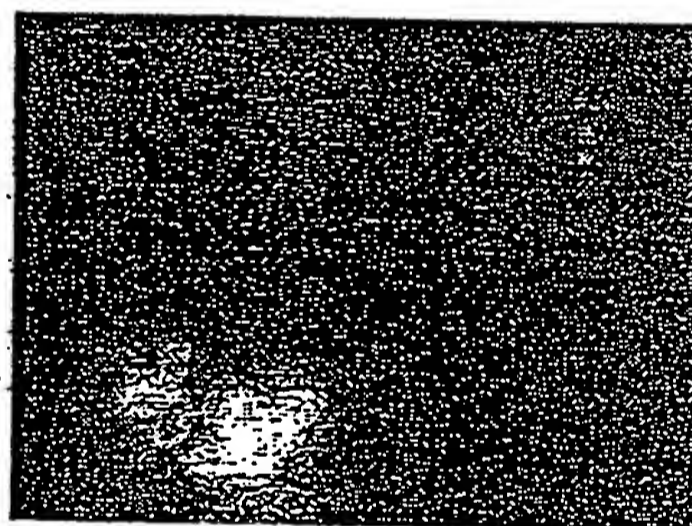
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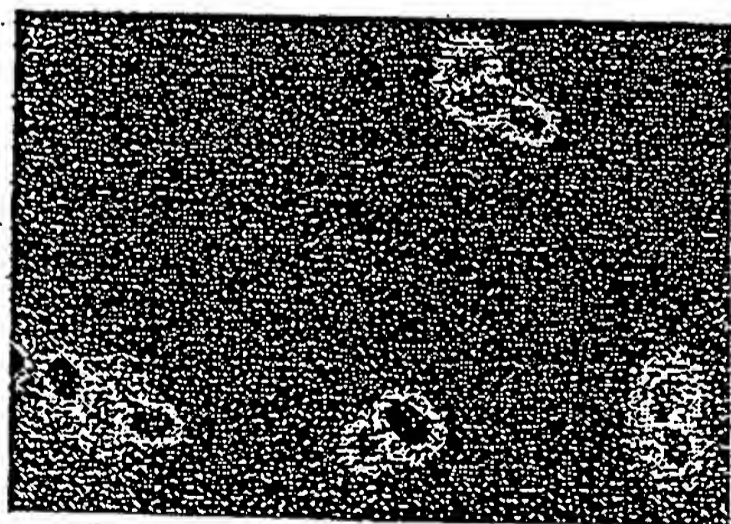


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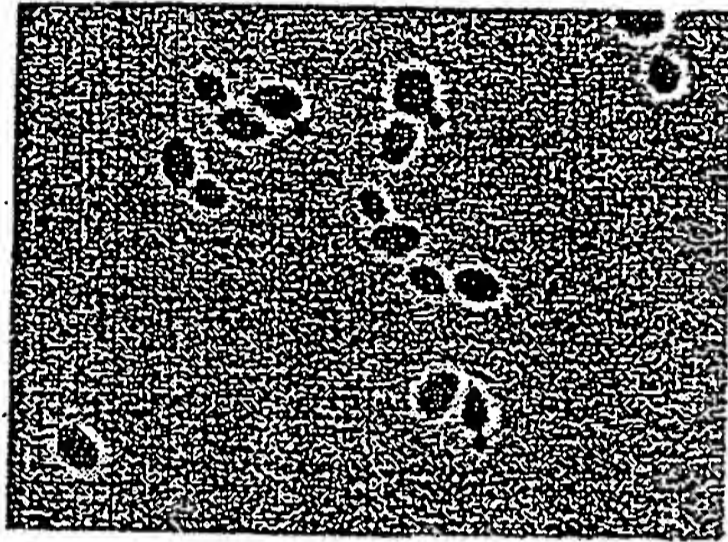
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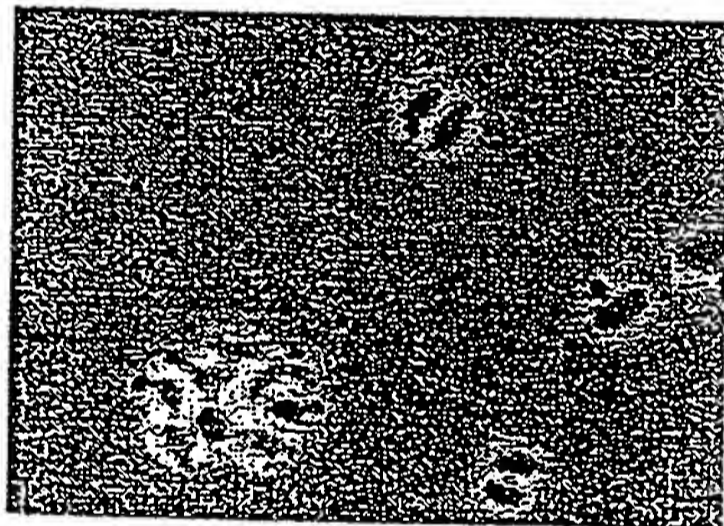
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Figure 20



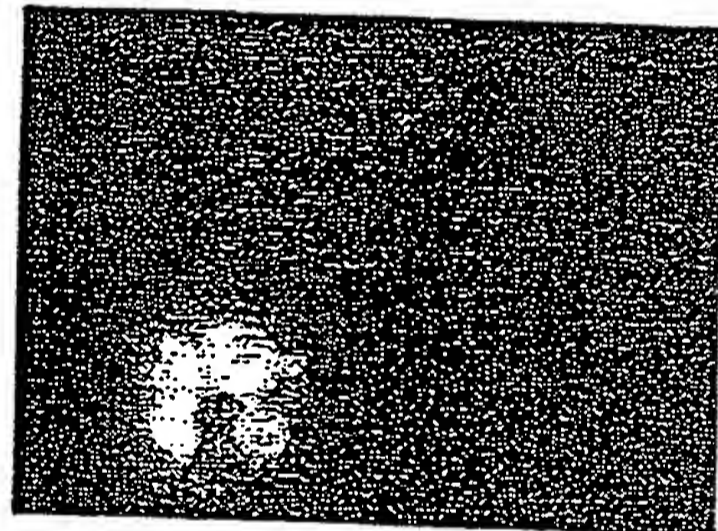
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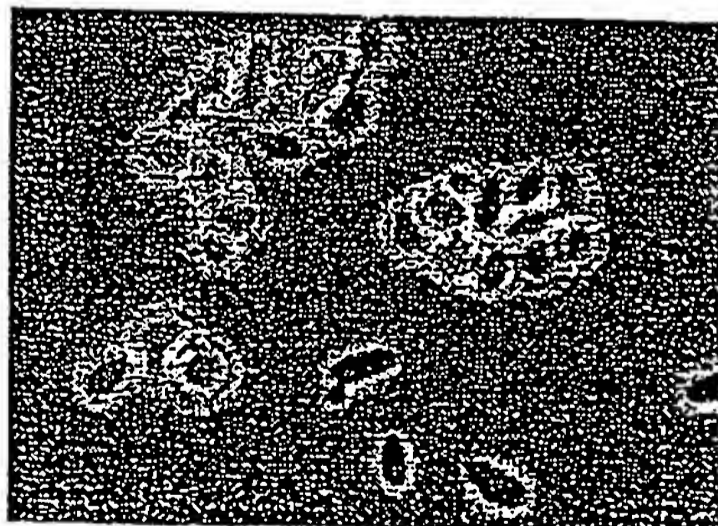


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A. CLASSIFICATION OF SUBJECT MATTER

IPC 5 C12N15/62 C12N1/19 C12N1/20 C12N11/16 //C12N1:19,
C12R1:465

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 5 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP,A,0 244 221 (GENENTECH, INC;US) 4 November 1987	1,2,4,5, 7,9-16
Y	see the whole document ---	8
X	WO,A,92 20805 (PIERRE FABRE MEDICAMENT) 26 November 1992	1,2,5,7, 9-14,16
Y	see the whole document ---	8
Y	WO,A,92 04363 (THE SALK INSTITUTE FOR BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES, INC.;US) 19 March 1992 See the abstract ---	8
P,X	WO,A,94 01567 (UNILEVER PLC,GB) 20 January 1994 cited in the application see the whole document ---	1-16
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Date of the actual completion of the international search

25 May 1994

Date of mailing of the international search report

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